

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:04:53 ; Search time 80.6667 Seconds
(without alignments)
28.767 Million cell updates/sec

Title: US-10-774-147B-30

Perfect score: 35

Sequence: 1 MKYHKM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: geneseq_16dec04:*
- 2: geneseqp1980s:*
- 3: geneseqp190s:*
- 4: geneseqp200s:*
- 5: geneseqp2001s:*
- 6: geneseqp2002s:*
- 7: geneseqp2003s:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	ADR44749	Adr44749 Human leu
2	31	88.6	886	AB891122	Abb91122 Herblcida
3	30	85.7	6	ADR44743	Adr44743 Human leu
4	30	85.7	6	ADR44737	Adr44737 Human leu
5	30	85.7	54	AAU17915	Aau17915 Novel hum
6	30	85.7	54	ADG41295	Adg41295 Human res
7	30	85.7	54	ADI97069	Adi97069 Human res
8	30	85.7	79	AA635466	Aag35466 Arabidops
9	30	85.7	114	ABP07404	Abp07404 Human ORF

10	30	85.7	125	3	AAG35465	Aag35465 Arabidops
11	30	85.7	140	3	AAG35464	Aag35464 Arabidops
12	30	85.7	153	3	AA621898	Aag21898 Arabidops
13	30	85.7	153	3	AA615863	Aag15863 Arabidops
14	30	85.7	153	3	AA653000	Aag53000 Arabidops
15	30	85.7	190	3	AA636085	Aab36085 Human DSP
16	30	85.7	190	4	AA673220	Aab73220 Human pho
17	30	85.7	190	4	AA678868	Aam78868 Human pro
18	30	85.7	190	6	AB672175	Abg72175 Human MAP
19	30	85.7	199	4	AA679852	Aam79852 Human pro
20	30	85.7	206	3	AA615862	Aag15862 Arabidops
21	30	85.7	206	3	AA621897	Aag21897 Arabidops
22	30	85.7	206	3	AA652999	Aag52999 Arabidops
23	30	85.7	215	3	AA615861	Aag15861 Arabidops
24	30	85.7	215	3	AA621896	Aag21896 Arabidops
25	30	85.7	215	3	AA652998	Aag52998 Arabidops
26	30	85.7	217	8	ADN22861	Adn22861 Bacterial
27	30	85.7	245	3	AA619287	Aag19287 Arabidops
28	30	85.7	258	4	AB669297	Abb69297 Drosophill
29	30	85.7	277	4	AA659393	Aab59393 Murine pr
30	30	85.7	306	6	ABU16944	Abu16944 Protein e
31	30	85.7	315	6	ADA33577	Ada33577 Acinetoba
32	30	85.7	333	4	AA678291	Aag78291 Mouse CD4
33	30	85.7	338	7	AD686481	Adh66481 Enterococ
34	30	85.7	439	3	AA619286	Aag19286 Arabidops
35	30	85.7	444	3	AA619285	Aag19285 Arabidops
36	30	85.7	449	3	AA622958	Aag22958 Arabidops
37	30	85.7	463	3	AA652216	Aag52216 Arabidops
38	30	85.7	467	3	AA640087	Aag40087 Arabidops
39	30	85.7	467	3	AA641408	Aag41408 Arabidops
40	30	85.7	467	3	AA622957	Aag22957 Arabidops
41	30	85.7	485	2	AA601459	Aa601459 Arabidops
42	30	85.7	485	3	AA640086	Aag40086 Arabidops
43	30	85.7	485	3	AA641407	Aag41407 Arabidops
44	30	85.7	485	7	ADP75199	Adp75199 Thale cre
45	30	85.7	485	8	ADN72983	Adn72983 Thale cre

ALIGNMENTS

RESULT 1	
ADR44749	
ID	ADR44749 standard; peptide; 6 AA.
XX	
AC	ADR44749;
XX	
DT	04-NOV-2004 (first entry)
XX	
DE	Human leukocyte stimulating peptide, P19.
XX	
KW	Arachidonic acid release; AA release; intracellular calcium release;
KW	immune response; pathogen; infectious disease;
KW	acquired immune deficiency syndrome; AIDS; cancer; gene therapy;
KW	leukocyte stimulating peptide; human.
XX	
OS	Homo sapiens.

XX	Herbicideally active polypeptide SEQ ID NO 333.
XX	KM Herbicideal; plant; agriculture; herbicide.
OS	Arabidopsis thaliana.
PN	WO200210210-A2.
PD	07-FEB-2002.
PF	28-AUG-2001; 2001WO-EPO09892.
XX	28-AUG-2001; 2001WO-EPO09892.
XX	(FARB) BAYER AG.
PA	Tietjen K, Weideler M;
PI	WPI; 2002-265010/31.
DR	Identifying plant target proteins for herbicideally active compounds,
PT	comprising aligning and comparing nucleic acid or amino acid sequences
PT	from plant with nucleic acid or amino acid sequences from non-plant
PT	organisms.
PS	Claim 5; SEQ ID NO 333; 261pp + Sequence Listing; English.
XX	
CC	The invention relates to identifying target proteins (ABB90790-ABB94016)
CC	for herbicideally active compounds, comprising aligning and comparing
CC	nucleic acid or amino acid sequences from plant with nucleic acid or
CC	amino acid sequences from non-plant organisms using suitable search
CC	parameters, where plant sequences having an E-value greater by a factor
CC	of 3 than the E-value of most similar non-plant sequences are selected.
CC	The polypeptides or nucleic acids encoding them are useful for
CC	identifying modulators. The identified modulators are useful as
CC	herbicides
XX	
SQ	Sequence 886 AA;
XX	
Query Match	88.6%; Score 31; DB 5; Length 886;
Best Local Similarity	83.3%; Pred. No. 6.4e+02;
Matches 5; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
QY	1 MKRYHQM 6 I::IIIII
Db	487 MQYHQM 492

Search completed: September 29, 2005, 12:31:11
Job time : 80.6667 secs

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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:04:53 ; Search time 80.6667 Seconds
(without alignments)
28.767 Million cell updates/sec

Title: US-10-774-147B-30
Perfect score: 35
Sequence: 1 MKYHKM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	8	ADR44749 Human leu
2	31	88.6	886	5	ABP91122 Herbicida
3	30	85.7	6	8	ADR44743 Human leu
4	30	85.7	6	8	ADR44737 Human leu
5	30	85.7	54	4	AAU17915 Novel hum
6	30	85.7	54	7	ADG41295 Human ros
7	30	85.7	54	7	AD197069 Human res
8	30	85.7	79	3	AA635466 Arabidops
9	30	85.7	114	5	ABP07404 Human ORF
10	30	85.7	125	3	AA635465 Arabidops
11	30	85.7	140	3	AA635464 Arabidops
12	30	85.7	153	3	AA621898 Arabidops
13	30	85.7	153	3	AA615863 Arabidops
14	30	85.7	153	3	AA653000 Arabidops
15	30	85.7	190	3	AA636085 Human DSP

16	30	85.7	190	4	AA673220 Human pho
17	30	85.7	190	4	AA678868 Human pro
18	30	85.7	190	6	ABG72175 Human MAP
19	30	85.7	199	4	AA679852 Human pro
20	30	85.7	206	3	AA615862 Arabidops
21	30	85.7	206	3	AA621897 Arabidops
22	30	85.7	206	3	AA652999 Arabidops
23	30	85.7	215	3	AA615861 Arabidops
24	30	85.7	215	3	AA621896 Arabidops
25	30	85.7	215	3	AA652998 Arabidops
26	30	85.7	217	8	ADN22861 Bacterial
27	30	85.7	245	3	AA619287 Arabidops
28	30	85.7	258	4	AB669297 Drosophi
29	30	85.7	277	4	AA659393 Murine pr
30	30	85.7	306	6	ABU16944 Protein e
31	30	85.7	315	6	ADA33577 Acinetoba
32	30	85.7	333	4	AA678291 Mouse CM
33	30	85.7	338	7	ADH66481 Enterococ
34	30	85.7	439	3	AA619286 Arabidops
35	30	85.7	444	3	AA619285 Arabidops
36	30	85.7	449	3	AA622958 Arabidops
37	30	85.7	463	3	AA652216 Arabidops
38	30	85.7	467	3	AA640087 Arabidops
39	30	85.7	467	3	AA641408 Arabidops
40	30	85.7	467	3	AA622957 Arabidops
41	30	85.7	485	2	AA601459 Arabidops
42	30	85.7	485	3	AA640086 Arabidops
43	30	85.7	485	3	AA641407 Arabidops
44	30	85.7	485	7	ADF51199 Thale cro
45	30	85.7	485	8	ADN72983 Thale cro

ALIGNMENTS

RESULT 1				
ID	ADR44749	standard; peptide; 6 AA.		
XX	AC			
XX	ADR44749;			
DT	04-NOV-2004	(first entry)		
XX	DE	Human leukocyte stimulating peptide, p19.		
XX	KW	Arachidonic acid release; AA releaser; intracellular calcium release;		
KW	KW	immune response; pathogen; infectious disease;		
KW	KW	acquired immune deficiency syndrome; AIDS; cancer; gene therapy;		
XX	XX	leukocyte stimulating peptide; human.		
XX	OS	Homo sapiens.		
XX	XX			
FH	Key	Location/Qualifiers		
FT	Modified-site	6 /note="C-terminal amide"		
XX	XX			
PN	W02004069858-A2.			

XX 19-AUG-2004.
 PD 06-FEB-2004; 2004WO-KR000225.
 XX 07-FEB-2003; 2003US-045621P.
 PF (POSC-) POSCO.
 XX (POST-) POSTECH FOUND.
 PA Ryu S, Bae Y, Park E, Suh P;
 XX WPI; 2004-60410/58.
 DR
 XX New leukocyte stimulating polypeptides useful for stimulating arachidonic
 PT acid release in target cells or for causing intracellular calcium
 PT release, and in gene therapy applications, such as to enhance immune
 PT response to bacteria.
 XX
 PS Claim 1; SEQ ID NO 30; 57pp; English.
 XX
 CC The present invention relates to a target cell stimulating peptide where
 CC the target cell may be a leukocyte or a phagocyte. The invention is
 CC useful for stimulating arachidonic acid (AA) and intracellular calcium
 CC release in human leukocytic cells and for superoxide generation in human
 CC neutrophils. The invention is also used to enhance immune response to
 CC pathogens such as bacteria and viruses and in the treatment of infectious
 CC diseases such as acquired immune deficiency syndrome (AIDS) and cancer.
 CC The invention is also useful in gene therapy. The present sequence is
 CC human leukocyte stimulating peptide. This sequence is used in the
 CC invention.
 CC
 SQ Sequence 6 AA;
 XX
 Query Match 100.0%; Score 35; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYHKM 6
 | | | | |
 Db 1 MKYHKM 6

RESULT 2
 ABB91122
 ID ABB91122 standard; protein; 886 AA.
 XX
 AC ABB91122;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Herbicidally active polypeptide SEQ ID NO 33.
 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX

PN WO200210210-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 28-AUG-2001; 2001WO-EP009892.
 XX 28-AUG-2001; 2001WO-EP009892.
 XX (FARB) BAYER AG.
 XX
 PA Tietjen K, Weidler M;
 XX WPI; 2002-269010/31.
 DR
 XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms.
 XX
 PS Claim 5; SEQ ID NO 333; 261pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 CC
 SQ Sequence 886 AA;
 XX
 Query Match 88.6%; Score 31; DB 5; Length 886;
 Best Local Similarity 83.3%; Pred. No. 6.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYHKM 6
 | | | | |
 Db 487 MQYHKM 492

Search completed: September 29, 2005, 12:31:11
 Job time : 80.6667 secs

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OM protein - protein search, using sw model
 Run on: September 29, 2005, 12:15:33 ; Search time 20.6667 Seconds
 (without alignments) 21.672 Million cell updates/sec
 Title: US-10-774-147B-30

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	88.6	583	4	US-09-248-796A-20244	Sequence 20244, A
2	30	85.7	140	3	US-08-930-894-4	Sequence 4, Appl1
3	30	85.7	277	2	US-08-683-992-30	Sequence 30, Appl1
4	30	85.7	277	2	US-09-144-923-30	Sequence 30, Appl1
5	30	85.7	315	4	US-09-328-352-4864	Sequence 4864, Ap
6	30	85.7	338	4	US-09-134-000C-4366	Sequence 4366, Ap
7	30	85.7	444	4	US-09-248-796A-19173	Sequence 19173, A
8	30	85.7	463	4	US-10-067-443-3	Sequence 3, Appl1
9	30	85.7	643	4	US-09-270-767-40779	Sequence 40779, A
10	30	85.7	643	4	US-09-270-767-55995	Sequence 55995, A
11	29	82.9	312	4	US-09-248-796A-14231	Sequence 14231, A
12	29	82.9	418	4	US-09-543-681A-7378	Sequence 7378, Ap
13	29	82.9	423	4	US-09-270-767-46381	Sequence 46381, A
14	28	80.0	96	4	US-09-270-767-32375	Sequence 32375, A
15	28	80.0	380	4	US-09-248-796A-21305	Sequence 21305, A
16	27	77.1	146	4	US-09-270-767-42622	Sequence 42622, A
17	27	77.1	151	4	US-09-270-767-45274	Sequence 45274, A
18	27	77.1	174	4	US-09-902-540-11679	Sequence 11679, A
19	27	77.1	178	3	US-09-134-001C-3908	Sequence 3908, Ap
20	27	77.1	220	4	US-09-710-279-1864	Sequence 1864, Ap
21	27	77.1	260	4	US-09-248-796A-18584	Sequence 18584, A
22	27	77.1	270	2	US-08-978-404B-8	Sequence 8, Appl1
23	27	77.1	273	2	US-08-978-404B-3	Sequence 3, Appl1

24	27	77.1	273	2	US-08-978-404B-6	Sequence 6, Appl1
25	27	77.1	313	4	US-09-543-681A-6835	Sequence 6835, Ap
26	27	77.1	376	4	US-09-248-796A-16143	Sequence 16143, A
27	27	77.1	421	4	US-09-198-452A-932	Sequence 932, Ap
28	27	77.1	421	4	US-09-438-185A-869	Sequence 869, Ap
29	27	77.1	433	4	US-09-328-352-6503	Sequence 6503, Ap
30	27	77.1	677	3	US-08-480-640A-115	Sequence 115, Ap
31	27	77.1	677	3	US-08-480-640A-193	Sequence 193, Ap
32	27	77.1	677	3	US-08-295-802-115	Sequence 115, Ap
33	27	77.1	677	3	US-08-686-968C-58	Sequence 58, Appl
34	27	77.1	677	3	US-08-686-968C-193	Sequence 193, Ap
35	27	77.1	677	3	US-08-488-237A-115	Sequence 115, Ap
36	27	77.1	677	3	US-08-488-237A-193	Sequence 193, Ap
37	27	77.1	677	3	US-08-375-992A-115	Sequence 115, Ap
38	27	77.1	677	3	US-08-375-992A-193	Sequence 193, Ap
39	27	77.1	677	4	US-08-472-679H-115	Sequence 115, Ap
40	27	77.1	677	4	US-08-472-679H-193	Sequence 193, Ap
41	27	77.1	677	4	US-09-902-540-16113	Sequence 16113, A
42	27	77.1	773	4	US-09-949-016-10285	Sequence 10285, A
43	27	77.1	780	4	US-09-949-016-6372	Sequence 6372, Ap
44	27	77.1	861	4	US-09-826-312A-10	Sequence 10, Appl
45	27	77.1	861	4	US-09-542-457A-10	Sequence 10, Appl

Search completed: September 29, 2005, 12:42:01
Job time : 20.6667 secs

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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:23:19 ; Search time 76.5 Seconds
(without alignments)
32.558 Million cell updates/sec

Title: US-10-774-147B-30
Perfect score: 35
Sequence: 1 MKYHKM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*\n1: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pdb:*\n2: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pdb:*

3: /cgn2_6/ptodate/1/pubpaa/US06_NEW_PUB pep:++
4: /cgn2_6/ptodate/1/pubpaa/US06_PUBCOMB pep:++
5: /cgn2_6/ptodate/1/pubpaa/US07_NEW_PUB pep:++
6: /cgn2_6/ptodate/1/pubpaa/PCTUS_PUBCOMB pep:++
7: /cgn2_6/ptodate/1/pubpaa/US08_NEW_PUB pep:++
8: /cgn2_6/ptodate/1/pubpaa/US08_PUBCOMB pep:++
9: /cgn2_6/ptodate/1/pubpaa/US09A_PUBCOMB pep:++
10: /cgn2_6/ptodate/1/pubpaa/US09B_PUBCOMB pep:++
11: /cgn2_6/ptodate/1/pubpaa/US09C_PUBCOMB pep:++
12: /cgn2_6/ptodate/1/pubpaa/US09_NEW_PUB pep:++
13: /cgn2_6/ptodate/1/pubpaa/US10A_PUBCOMB pep:++
14: /cgn2_6/ptodate/1/pubpaa/US10B_PUBCOMB pep:++
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17: /cgn2_6/ptodate/1/pubpaa/US10E_PUBCOMB pep:++
18: /cgn2_6/ptodate/1/pubpaa/US10E_NEW_PUB pep:++
19: /cgn2_6/ptodate/1/pubpaa/US11A_PUBCOMB pep:++
20: /cgn2_6/ptodate/1/pubpaa/US11_NEW_PUB pep:++
21: /cgn2_6/ptodate/1/pubpaa/US60_NEW_PUB pep:++
22: /cgn2_6/ptodate/1/pubpaa/US60_PUBCOMB pep:++

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	16	US-10-774-147B-30
2	30	85.7	6	16	US-10-774-147B-18
3	30	85.7	6	16	US-10-774-147B-24
4	30	85.7	54	9	US-09-764-860-533
5	30	85.7	54	14	US-10-074-095-533
6	30	85.7	54	15	US-10-212-872-533
7	30	85.7	182	16	US-10-767-701-47283
8	30	85.7	183	15	US-10-424-599-233688
9	30	85.7	186	16	US-10-425-115-214464
10	30	85.7	187	15	US-10-052-648A-81
11	30	85.7	189	14	US-10-087-887-94
12	30	85.7	190	13	US-10-044-205A-42
13	30	85.7	190	13	US-10-044-205A-44
14	30	85.7	190	14	US-10-087-887-95
15	30	85.7	190	15	US-10-052-648A-82
16	30	85.7	217	15	US-10-369-493-5514
17	30	85.7	258	20	US-11-097-143-34683
18	30	85.7	306	15	US-10-282-122A-44868
19	30	85.7	311	16	US-10-739-930-9673
20	30	85.7	333	9	US-09-788-626-31
21	30	85.7	371	15	US-10-424-599-285296
22	30	85.7	463	14	US-10-067-443-3
23	30	85.7	463	15	US-10-649-273-3
24	30	85.7	463	15	US-10-651-722-3
25	30	85.7	721	20	US-11-097-143-16797
26	30	85.7	822	16	US-10-437-963-112463
27	30	85.7	962	15	US-10-366-547-85

ALIGNMENTS

28	30	85.7	1153	16	US-10-367-094-116	Sequence 116, App
29	30	85.7	1291	15	US-10-366-547-83	Sequence 83, Appl
30	29	82.9	6	16	US-10-774-147B-32	Sequence 32, Appl
31	29	82.9	139	14	US-10-087-887-100	Sequence 100, Appl
32	29	82.9	151	15	US-10-052-648A-80	Sequence 80, Appl
33	29	82.9	152	15	US-10-275-762-68	Sequence 68, Appl
34	29	82.9	166	15	US-10-275-762-67	Sequence 67, Appl
35	29	82.9	177	9	US-09-864-761-42750	Sequence 42750, A
36	29	82.9	188	14	US-10-181-590-6	Sequence 6, Appl
37	29	82.9	188	14	US-10-087-887-18	Sequence 18, Appl
38	29	82.9	188	15	US-10-094-749-2359	Sequence 2359, Ap
39	29	82.9	188	15	US-10-052-648A-30	Sequence 30, Appl
40	29	82.9	188	15	US-10-052-648A-78	Sequence 78, Appl
41	29	82.9	188	15	US-10-052-648A-79	Sequence 79, Appl
42	29	82.9	192	9	US-09-764-869-872	Sequence 872, App
43	29	82.9	192	14	US-10-091-504-872	Sequence 547, App
44	29	82.9	192	14	US-10-103-313-547	Sequence 872, App
45	29	82.9	192	15	US-10-227-577-872	Sequence 872, App

RESULT 1
US-10-774-147B-30
Sequence 30, Application US/10774147B
Publication No. US20040248255A1
GENERAL INFORMATION:
APPLICANT: POSTECH Foundation
APPLICANT: RYU, Sung-Ho
APPLICANT: BAE, Yoo-Sik
APPLICANT: PARK, Eun-Young
APPLICANT: SUH, Pann-Gh11
TITLE OF INVENTION: LEUKOCYTE STIMULATING PEPTIDES
FILE REFERENCE: 10050-03USA
CURRENT APPLICATION NUMBER: US/10/774,147B
PRIOR FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US 60/445, 621
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: Peptide
LOCATION: (1)..(6)
OTHER INFORMATION: P19
US-10-774-147B-30
Query Match 100.0%; Score 35; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MKYHKM 6
| | | | |
Db 1 MKYHKM 6
Search completed: September 29, 2005, 12:49:47
Job time : 76.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:13:23 ; Search time 14.5 Seconds
(without alignments)
39.814 Million cell updates/sec

Title: US-10-774-147B-30

Perfect score: 35

Sequence: 1 MKYHKM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	88.6	64	2 T34160	hypothetical prote
2	31	88.6	558	2 T32028	hypothetical prote
3	30	85.7	69	2 D72657	AcOrf-59 protein -
4	30	85.7	161	2 AC0439	conserved hypothet
5	30	85.7	171	2 T41803	AcIMPV orf58 - Bom
6	30	85.7	217	2 T20339	hypothetical prote

7	30	85.7	237	2 A69490	ISU ribosomal prot
8	30	85.7	259	2 T11068	cytochrome-c oxida
9	30	85.7	314	2 G90191	conserved hypothet
10	30	85.7	435	2 T49082	hypothetical prote
11	30	85.7	463	2 E84888	probable O-6-alogl
12	30	85.7	485	2 C71400	adenosylhomocystei
13	30	85.7	535	2 S56946	probable membrane
14	30	85.7	580	2 T28725	hypothetical prote
15	30	85.7	754	2 S52816	probable membrane
16	30	85.7	1273	1 TDR1T	leukocyte common a
17	30	85.7	1291	1 A28334	protein-tyrosine-p
18	30	85.7	1652	2 T16799	hypothetical prote
19	29	82.9	242	2 E71621	ERCC1-like excisio
20	29	82.9	328	2 T28363	ORF MSV202 hypot
21	29	82.9	442	2 T37733	hypothetical zinc
22	29	82.9	447	2 T19112	hypothetical prote
23	28	80.0	166	2 T06580	hypothetical prote
24	28	80.0	260	2 T28182	hypothetical prote
25	28	80.0	315	2 T05512	hypothetical prote
26	28	80.0	325	2 T00161	leucocidin chain F
27	28	80.0	325	2 S32212	leucocidin chain F
28	28	80.0	480	2 B45600	asparagine-rich bl
29	28	80.0	642	2 G82886	topoisomerase IV s
30	28	80.0	642	2 D90558	topoisomerase IV s
31	28	80.0	1030	2 S73460	probable helicase
32	28	80.0	3394	2 T18501	hypothetical prote
33	27	77.1	65	2 AF1590	hypothetical prote
34	27	77.1	65	2 AG1649	hypothetical prote
35	27	77.1	150	2 T23684	hypothetical prote
36	27	77.1	189	2 T30408	hypothetical prote
37	27	77.1	189	2 C89992	hypothetical prote
38	27	77.1	207	2 G70198	hypothetical prote
39	27	77.1	209	1 S48459	probable dual spec
40	27	77.1	217	1 B44570	3-oxoadipate CoA-t
41	27	77.1	229	2 A89997	hypothetical prote
42	27	77.1	256	2 B81691	conserved hypothet
43	27	77.1	256	2 C71536	hypothetical prote
44	27	77.1	270	2 S56160	mast cell tryptase
45	27	77.1	273	2 A47246	tryptase (EC 3.4.2

Search completed: September 29, 2005, 12:39:50
Job time : 14.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:11:58 ; Search time 70 Seconds
(without alignments)
43.893 Million cell updates/sec
Title: US-10-774-147B-30
Perfect score: 35
Sequence: 1 MKYHKM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database :
1: uniprot_sprot:;
2: uniprot_trembl:;

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	485	1	SAHH_PETCR
2	32	91.4	83	2	Q76VH3
3	32	91.4	191	2	Q70S81
4	32	91.4	962	2	Q9DJT3
5	32	91.4	1069	2	Q6B156
6	32	91.4	3452	1	ASPM_CANFA
7	31	88.6	121	2	Q9MCC4
8	31	88.6	121	2	Q9KQ05
9	31	88.6	218	2	Q8T2Q1
10	31	88.6	276	1	IBP2_BRARE
11	31	88.6	558	2	Q16656
12	31	88.6	631	2	Q9XD02
13	31	88.6	886	2	Q9FYK0
14	31	88.6	924	2	Q9FXJ6
15	30	85.7	69	1	Y059_NPVAC
16	30	85.7	121	2	Q8C3M6
17	30	85.7	128	2	Q7YY19
18	30	85.7	161	2	Q8ZB19
19	30	85.7	171	2	Q92A24
20	30	85.7	172	2	Q8B9J2
21	30	85.7	189	2	Q9DD06
22	30	85.7	190	1	DUSL_HUMAN
23	30	85.7	190	2	Q9Y346
24	30	85.7	215	2	Q8L009
25	30	85.7	215	2	Q8LW11
26	30	85.7	217	2	Q9LJ88
27	30	85.7	229	2	Q18969
28	30	85.7	237	1	R12_ARCTU
29	30	85.7	238	1	R12_METAC

ALIGNMENTS

RESULT 1
SAHH_PETCR
ID SAHH_PETCR STANDARD: PRT; 485 AA.
AC Q01781;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine
hydrolase) (AdoHcyase).
GN Name=SAHH; Synonyms=SHH;
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Campanulids; Apiales; Apiaceae; Apioideae; apioid superclade;
OC Apium clade; Petroselinum.
OX NCBI_TaxID=4043;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=92262510; PubMed=1374911;
RA Kewalleck P., Plesch G., Hahlbrock K., Somsich I.E.;
RT "Induction by fungal elicitor of S-adenosyl-L-methionine synthetase
and S-adenosyl-L-homocysteine hydrolase mRNAs in cultured cells and
leaves of Petroselinum crispum.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4713-4717(1992).
RN [2]
RP SEQUENCE OF 259-485 FROM N.A.
RA Somsich I.E., Bollmann U., Hahlbrock K., Kombrink E., Schulz W.;
RT "Differential early activation of defense-related genes in elicitor-
treated parsley cells.";
RL Plant Mol. Biol. 12:227-234(1989).
CC -I- FUNCTION: Adenosylhomocysteine is a competitive inhibitor of S-
adenosyl-L-methionine-dependent methyl transferase reactions;
CC therefore adenosylhomocysteine may play a key role in the
CC control of methylations via regulation of the intracellular
CC concentration of adenosylhomocysteine.

30 30 85.7 238 1 R12_METYA Q8PV47 methanosarc
31 30 85.7 240 2 Q6FV58 Q6FV58 candida gl
32 30 85.7 258 2 Q9VFX4 Q9VFX4 diosopilla
33 30 85.7 259 2 Q47576 Q47576 onchocerca
34 30 85.7 259 2 Q8BN50 Q8BN50 brugia mala
35 30 85.7 286 2 Q74M16 Q74M16 lactobacill
36 30 85.7 306 2 Q833M3 Q833M3 enterococcu
37 30 85.7 314 2 Q972V8 Q972V8 sulfolobus
38 30 85.7 378 2 Q65A84 Q65A84 caenorhabd
39 30 85.7 422 2 Q6X0R6 Q6X0R6 onion yello
40 30 85.7 435 2 Q9SV01 Q9SV01 arabidopsi
41 30 85.7 445 2 Q7RH06 Q7RH06 plasmidum
42 30 85.7 480 2 Q22145 Q22145 arabidopsi
43 30 85.7 485 1 SAHH_ARATH Q23255 arabidopsi
44 30 85.7 485 2 Q8LE20 Q8LE20 arabidopsi
45 30 85.7 485 2 Q8LPS8 Q8LPS8 arabidopsi

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-homocysteine + adenosine.
 CC -1- COFACTOR: Binds 1 NAD per subunit.
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- TISSUE SPECIFICITY: Mainly in floral buds and stems.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteinase family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M81885; AAA33855.1; -.
 CC EMBL: M62756; AAA33855.1; -.
 CC PIR: T15035; T15035.
 CC HSP: P23526; 1L14.
 CC InterPro: IPR000043; Ad_hcy_hydrolase.
 CC Pfam: PF05221; AdoHcyase; 1.
 CC Pfam: PF00670; AdoHcyase; 1.
 CC TIGRfams: TIGR00936; ahcy; 1.
 CC PROSITE: PS00738; ADOHCYASE_1; 1.
 CC PROSITE: PS00739; ADOHCYASE_2; 1.
 CC KEGG: Hydrolase; NAD; One-carbon metabolism.
 CC FT DOMAIN 232 401 NAD binding (By similarity).
 CC FT BINDING 64 64 Substrate (By similarity).
 CC FT BINDING 139 139 Substrate (By similarity).
 CC FT BINDING 205 205 Substrate (By similarity).
 CC FT BINDING 235 235 Substrate (By similarity).
 CC FT BINDING 239 239 Substrate (By similarity).
 CC FT CONFLICT 346 346 C -> D (in Ref. 1; AAA33855).
 CC FT CONFLICT 439 439 L -> C (in Ref. 1; AAA33855).
 CC SQ SEQUENCE 485 AA: 53181 MW: 95926516c2e08e6 CRC64,

Query Match 100.0%; Score 35; DB 1; Length 485;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYHKM 6
 |||||
 DB 190 MKYHKM 195

Search completed: September 29, 2005, 12:38:17
 Job time : 71 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:04:53 ; Search time 80.6667 Seconds
(without alignments)
28.767 Million cell updates/sec

Title: US-10-774-147B-31

Perfect score: 34

Sequence: 1 MKYHM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	6	ADR44750	Adr44750 Human leu
2	34	100.0	109	AAU16530	Aau16530 Human nov
3	34	100.0	109	ABU55599	Abu55599 Human nov
4	34	100.0	280	ABR99912	Abbr99912 Human mac
5	34	100.0	366	AAU16107	Aau16107 Human nov
6	34	100.0	366	ABU55176	Abu55176 Human nov
7	34	100.0	480	ABP69649	Abp69649 Human pol
8	34	100.0	490	AAO16430	Aao16430 Human nuc
9	34	100.0	534	ADG42180	Adg42180 Human bra

10	34	100.0	567	ADAS5339	Ada55339 Human pro
11	31	91.2	298	AAg17193	Aagi7193 Arabidops
12	31	91.2	298	AAc06493	Aac06493 Arabidops
13	31	91.2	298	AAg42865	Aag42865 Arabidops
14	31	91.2	307	AAc06492	Aac06492 Arabidops
15	31	91.2	307	AAg17192	Aagi7192 Arabidops
16	31	91.2	307	AAg42864	Aag42864 Arabidops
17	31	91.2	331	AAy67405	Aay67405 Arabidops
18	31	91.2	406	AAW88440	Aaw88440 Arabidops
19	31	91.2	406	AAy67409	Aay67409 Arabidops
20	31	91.2	406	AAc06491	Aac06491 Arabidops
21	31	91.2	406	AAg42863	Aag42863 Arabidops
22	31	91.2	406	AAg17191	Aagi7191 Arabidops
23	31	91.2	410	AAc21144	Aac21144 Arabidops
24	31	91.2	425	AAc21143	Aac21143 Arabidops
25	31	91.2	457	AAc21142	Aac21142 Arabidops
26	30	88.2	177	AAW55224	Aaw55224 Peptide #
27	30	88.2	177	ABB34215	Abb34215 Peptide #
28	30	88.2	177	AAW27685	Aaw27685 Peptide #
29	30	88.2	177	ABR29053	Abbr29053 Peptide #
30	30	88.2	177	AAW67394	Aaw67394 Human bon
31	30	88.2	177	AAW55008	Aaw55008 Human bra
32	30	88.2	177	ABG49053	Abg49053 Human liv
33	30	88.2	177	AAW02967	Aaw02967 Peptide #
34	30	88.2	177	ABG37020	Abg37020 Human pep
35	30	88.2	188	AAW19008	Aaw19008 A human d
36	30	88.2	188	AAW33221	Aaw33221 Human pho
37	30	88.2	188	AAW33223	Aaw33223 Human pol
38	30	88.2	188	AAW85360	Aaw85360 Human pho
39	30	88.2	188	ABW82163	Abw82163 Human NOV
40	30	88.2	188	ADAs4791	Adas4791 Human pro
41	30	88.2	188	ADW74734	Adw74734 Human tyr
42	30	88.2	188	ADW48580	Adw48580 Dual spec
43	30	88.2	192	AAU22098	Aau22098 Human car
44	30	88.2	192	AAU21820	Aau21820 Novel hum
45	30	88.2	192	AAW41109	Aaw41109 Human pol

ALIGNMENTS

RESULT 1
ADR44750
ID ADR44750 standard; peptide; 6 AA.
XX
AC ADR44750;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human leukocyte stimulating peptide, P20.
XX
KW Archidonic acid release; AA release; intracellular calcium release;
KW immune response; pathogen; infectious disease;
KW acquired immune deficiency syndrome; AIDS; cancer; gene therapy;
KW leukocyte stimulating peptide; human.
XX
OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Modified-site 6
FT /note="C-terminal amide"
XX
XX WO2004069858-A2.
XX PD 19-AUG-2004.
XX PF 06-FEB-2004; 2004WO-KR000225.
XX PR 07-FEB-2003; 2003US-0453621P.
XX PA (POSC-) POSCO.
XX PA (POST-) POSTECH FOUND.
XX PI Ryu S, Bae Y, Park E, Suh P;
XX DR WPI; 2004-604410/58.
XX PT New leukocyte stimulating polypeptides useful for stimulating arachidonic
PT acid release in target cells or for causing intracellular calcium
PT release, and in gene therapy applications, such as to enhance immune
PT response to bacteria.
XX PS Claim 1; SEQ ID NO 31; 57pp; English.
XX CC The present invention relates to a target cell stimulating peptide where
CC the target cell may be a leukocyte or a phagocyte. The invention is
CC useful for stimulating arachidonic acid (AA) and intracellular calcium
CC release in human leukocyte cells and for superoxide generation in human
CC neutrophils. The invention is also used to enhance immune response to
CC pathogens such as bacteria and viruses and in the treatment of infectious
CC diseases such as acquired immune deficiency syndrome (AIDS) and cancer.
CC The invention is also useful in gene therapy. The present sequence is
CC human leukocyte stimulating peptide. This sequence is used in the
CC invention.
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 34; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKRYHW 6
111111
Db 1 MKRYHW 6
RESULT 2
AAU16530
ID AAU16530 standard; protein; 109 AA.
XX AC AAU16530;
XX DT 07-NOV-2001 (first entry)
XX

DE Human novel secreted protein, Seq ID 1483.
XX
XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW cardiac; vasotropic; cerebroprotective; neuroprotective;
KW antibacterial; virucide; fungicide; opthalmological; vulnereary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX OS Homo sapiens.
XX PN WO200155322-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001341.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227039P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229309P.
PR 05-SEP-2000; 2000US-0229313P.
PR 06-SEP-2000; 2000US-0230337P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0232081P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259676P.
PA (HUMA-) HUMAN GENOME SCT INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-488783/53.
DR N-PDB: AAS26517.
XX
XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 11; SEQ ID NO 1483; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their

CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed

Query Match 100.0%; Score 34; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKYVM 6
|||
DB 11 MKYVM 16

RESULT 3
ID ABUS5599 standard; protein; 109 AA.

AC ABUS5599;

DT 18-MAR-2003 (first entry)

DE Human novel polypeptide #686.

XX Human; neural disorder; immune system disorder; renal disorder;

KW muscular disorder; respiratory disease; reproductive disorder;

KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;

KW hyperproliferative disorder; inflammatory disease; allergic reaction;

KW blood related disorder; cancer; immunosuppressive; antiinflammatory;

KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;

KW haemostatic; antiarteriosclerotic.

OS Homo sapiens.

XX US2002132753-A1.

XX 19-SEP-2002.

XX 17-JAN-2001; 2001US-00764864.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226668P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 27-SEP-2000; 2000US-0235634P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARAA/) BARASH S C.

XX PI Rosen CA, Ruben SM, Barash SC;
 XX DR WPI: 2003-147444/14.
 DR N-PSDB; ABX73858.
 XX PT New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.
 XX PS Claim 11; SEQ ID NO 1483; 402pp; English.
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABU54914-ABU55699 and
 CC ABU55748 represent human novel polypeptides of the invention
 XX SQ Sequence 109 AA;
 Query Match 100.0%; Score 34; DB 6; Length 109;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRYHM 6
 DB 11 MKRYHM 16
 RESULT 4
 ABB99912
 ID ABB99912 standard; protein; 280 AA.
 XX AC ABB99912;
 XX DT 30-JAN-2003 (first entry)
 XX DE Human macroprotein 1196-30.80.
 XX KW Human; macroprotein 1196-30.80; human KIAA1196 protein homologue;
 KW recombinant production; gene therapy; dementia; facial paralysis.
 XX OS Homo sapiens.
 XX PN CN1345807-A.
 XX

PD 24-APR-2002.
 XX 26-SEP-2000; 2000CN-00125427.
 PF 26-SEP-2000; 2000CN-00125427.
 XX 26-SEP-2000; 2000CN-00125427.
 PR (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX Mao Y, Xie Y;
 PI WPI: 2002-548942/59.
 DR N-PSDB; ABV76281.
 XX PT Novel polypeptide-human macroprotein 1196-30.80 and polynucleotide
 PT encoding the polypeptide.
 XX PS Claim 1; Page 26-27 (Disclosure); 33pp; Chinese.
 CC The invention relates to human macroprotein 1196-30.80 (ABB99912) and
 CC nucleic acids encoding it (ABV76281). The protein has a molecular weight
 CC of 30.8 kD and has 468 identity and 598 homology over a 176 amino acid
 CC stretch with human KIAA1196 protein (GenBank accession number AB033022).
 CC The invention also relates to a method for the recombinant production of
 CC the protein, an antagonist of the protein, and the use of the protein,
 CC gene and antagonist in therapeutic applications. Macroprotein 1196-30.80
 CC can be used in the treatment of a variety of diseases such as dementia
 CC and facial paralysis. The present sequence represents human macroprotein
 CC 1196-30.80
 XX SQ Sequence 280 AA;
 Query Match 100.0%; Score 34; DB 5; Length 280;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRYHM 6
 DB 184 MKRYHM 189
 RESULT 5
 AAU16107
 ID AAU16107 standard; protein; 366 AA.
 XX AC AAU16107;
 XX DT 07-NOV-2001 (first entry)
 XX DE Human novel secreted protein, Seq ID 1060.
 XX KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
 KW cardiac; vasotropic; cerebroprotective; neurotropic; neuroprotective;
 KW antibacterial; virucide; fungicide; opthalmological; vulnerary;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiogenesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW

KW	wound healing; epithelial cell proliferation; skin ageing; food additive;
XV	preservative; antiproliferative.
XX	
XX	Homo sapiens.
XX	WO20015532Z-A2.
XX	
PD	02-AUG-2001.
PF	17-JAN-2001; 2001WO-US001341.
XX	
XX	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0186456P.
PR	02-MAR-2000; 2000US-0186550P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	26-JUN-2000; 2000US-0214866P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216680P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
PR	14-JUL-2000; 2000US-0218290P.
PR	26-JUL-2000; 2000US-0220963P.
PR	26-JUL-2000; 2000US-0220964P.
PR	14-AUG-2000; 2000US-0224518P.
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PR	14-AUG-2000; 2000US-0225759P.
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PR	22-AUG-2000; 2000US-0226681P.
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PR	23-AUG-2000; 2000US-0227182P.
PR	23-AUG-2000; 2000US-0227009P.
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PR	06-SEP-2000; 2000US-0230438P.
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PR	
PR	08-SEP-2000; 2000US-0231244P.
PR	08-SEP-2000; 2000US-0231413P.
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PR	08-SEP-2000; 2000US-0232080P.
PR	08-SEP-2000; 2000US-0232081P.
PR	12-SEP-2000; 2000US-0231966P.
PR	14-SEP-2000; 2000US-0232397P.
PR	14-SEP-2000; 2000US-0232398P.
PR	14-SEP-2000; 2000US-0232399P.
PR	14-SEP-2000; 2000US-0232400P.
PR	14-SEP-2000; 2000US-0232401P.
PR	14-SEP-2000; 2000US-0233063P.
PR	14-SEP-2000; 2000US-0233064P.
PR	14-SEP-2000; 2000US-0233065P.
PR	21-SEP-2000; 2000US-0234223P.
PR	21-SEP-2000; 2000US-0234224P.
PR	21-SEP-2000; 2000US-0234277P.
PR	25-SEP-2000; 2000US-0234937P.
PR	25-SEP-2000; 2000US-0234998P.
PR	26-SEP-2000; 2000US-0234844P.
PR	27-SEP-2000; 2000US-0235834P.
PR	27-SEP-2000; 2000US-0235836P.
PR	29-SEP-2000; 2000US-0236327P.
PR	29-SEP-2000; 2000US-0236367P.
PR	29-SEP-2000; 2000US-0236368P.
PR	29-SEP-2000; 2000US-0236369P.
PR	29-SEP-2000; 2000US-0236370P.
PR	02-OCT-2000; 2000US-0236802P.
PR	02-OCT-2000; 2000US-0237037P.
PR	02-OCT-2000; 2000US-0237038P.
PR	02-OCT-2000; 2000US-0237039P.
PR	02-OCT-2000; 2000US-0237040P.
PR	13-OCT-2000; 2000US-0239935P.
PR	13-OCT-2000; 2000US-0239937P.
PR	20-OCT-2000; 2000US-0240960P.
PR	20-OCT-2000; 2000US-0241221P.
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PR	20-OCT-2000; 2000US-0241786P.
PR	20-OCT-2000; 2000US-0241787P.
PR	20-OCT-2000; 2000US-0241808P.
PR	20-OCT-2000; 2000US-0241809P.
PR	20-OCT-2000; 2000US-0241826P.
PR	01-NOV-2000; 2000US-0244617P.
PR	08-NOV-2000; 2000US-0246474P.
PR	08-NOV-2000; 2000US-0246475P.
PR	08-NOV-2000; 2000US-0246476P.
PR	08-NOV-2000; 2000US-0246477P.
PR	08-NOV-2000; 2000US-0246478P.
PR	08-NOV-2000; 2000US-0246523P.
PR	08-NOV-2000; 2000US-0246524P.
PR	08-NOV-2000; 2000US-0246

PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251889P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
FI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-488783/53.
DR N-PSDB; AAS26094.
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 11; SEQ ID NO 1060; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.

CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischemia, angiodenosis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
Query Match 100.0%; Score 34; DB 4; Length 366;
Best local similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKRYHM 6
|||||
Db 11 MKRYHM 16
RESULT 6
ABU5176
ID ABU5176 standard; protein; 366 AA.
XX
AC ABU5176;
XX
DT 18-MAR-2003 (first entry)
XX
DE Human novel polypeptide #263.
XX
KW Human; neural disorder; immune system disorder; renal disorder;
KW muscular disorder; respiratory disease; reproductive disorder;
KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW hyperproliferative disorder; inflammatory disorder; allergic reaction;
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
KW haemostatic; antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN US2002132753-A1.
XX
PD 19-SEP-2002.
XX
PR 17-JAN-2001; 2001US-00764864.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
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 PR 14-AUG-2000; 2000US-0224518P.
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 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225758P.
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 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
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 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
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 PR 25-SEP-2000; 2000US-0234897P.
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 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
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 XX
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-147444/14.
 DR N-PSDB; ABX73435.
 XX
 XX
 PT New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.

XX
 PS Claim 11; SEQ ID NO 1060; 402bp; English.
 XX
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABU54914-ABU55099 and
 CC ABU55748 represent human novel polypeptides of the invention
 CC
 SQ Sequence 366 AA;
 XX
 Query Match 100.0%; Score 34; DB 6; Length 366;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRYHM 6
 Db 11 MKRYHM 16
 II III I I I
 RESULT 7
 ABP69649
 ID ABP69649 standard; protein; 490 AA.
 XX
 AC ABP69649;
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 1696.
 XX
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
 KW antitartaric.
 XX
 OS Homo sapiens.
 XX
 PN WO200270539-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 05-MAR-2002; 2002WO-US005095.
 XX

PR 05-MAR-2001; 2001US-00799451.
 XX (HYSE-) HXSEQ INC.
 PA
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX WPI; 2002-759812/82.
 DR N-PSDB; ABZ11866.
 XX
 PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX
 PS Claim 9; SEQ ID NO 1696; 1012pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (1) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 490 AA;
 XX
 Query Match 100.0%; Score 34; DB 5; Length 490;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS;
 KW cancer; developmental disorder; renal tubular acidosis; anaemia; asthma;
 KW mental retardation; neurological disorder; Alzheimer's disease; epilepsy;
 KW Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;
 KW Crohn's disease; transgenic animal; animal model.
 XX
 OS Homo sapiens.
 XX
 PN WO200300864-A2.
 XX
 PD 03-JAN-2003.
 XX
 XX 20-JUN-2002; 2002WO-US021179.
 PF
 XX 22-JUN-2001; 2001US-0300518P.
 PR 29-JUN-2001; 2001US-0301787P.
 PR 29-JUN-2001; 2001US-0301792P.
 PR 29-JUN-2001; 2001US-0301892P.
 PR 29-JUN-2001; 2001US-0301893P.
 PR 06-JUL-2001; 2001US-0303405P.
 PR 06-JUL-2001; 2001US-0303442P.
 PR 15-MAR-2002; 2002US-0364438P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BW;
 PI Aryvzu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe J;
 PI Ramkumar J, Griffin JA, Yang J, Sanjennala MW, Baughn MR;
 PI Borowsky ML, Yao MG, Walla NK, Bandman O, Lal PG, Beecha SD, Lee SY;
 PI Richardson TW, Elliott VS, Luo W, Tang YT, Zebartjadian Y, Lu Y;
 XX WPI; 2003-201420/19.
 DR N-PSDB; AAL51580.
 XX
 PT New nucleic acid-associated proteins and polynucleotides, useful for
 PT diagnosing, treating or preventing cell proliferative (e.g. cancer),
 PT neurological (e.g. epilepsy or Parkinson's disease), or autoimmune
 PT disorders (e.g. AIDS).
 XX
 PS Claim 1; Page 257-258; 312pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human
 CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
 CC the invention are useful for diagnosing, treating or preventing disorders
 CC associated with aberrant expression of NAAP, such as: cell proliferative
 CC disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis
 CC or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia
 CC or mental retardation); neurological disorders (e.g. Alzheimer's disease,
 CC Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders
 CC (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of
 CC the invention are useful for creating transgenic animals to model human
 CC disease. The present amino acid sequence represents a human nucleic acid-
 CC associated protein of the invention
 XX
 SQ Sequence 490 AA;
 XX
 Query Match 100.0%; Score 34; DB 6; Length 490;

Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKYHVM 6
111111
Db 135 MKYHVM 140

RESULT 9

ID ADG42180
ADG42180 standard; protein; 534 AA.

AC ADG42180;

DT 26-FEB-2004 (first entry)

DE Human brain/hippocampus polypeptide #28.

KW Human; brain; hippocampus; protein chip; adult brain; foetal brain.

OS Homo sapiens.

PN JP2002330794-A.

PD 19-NOV-2002.

PF 25-APR-2001; 2002JP-00049081.

PR 25-APR-2001; 2001JP-00127066.

PA (KAZU-) 2H KAZUSA DNA KENKYUSHO.

DR WPI; 2003-460752/44.

DR N-PSDB; ADG42135.

PT Direct cloning and determination of base sequences of DNAs containing a

PT region encoding for proteins from cDNA libraries derived from whole human

PT adult and foetal brains, and human adult hippocampus.

PS Claim 1; SEQ ID NO 73; 183pp; Japanese.

CC The invention relates to cDNA libraries derived from whole human adult

CC and foetal brains and human adult hippocampus. The invention is useful

CC for preparation of recombinant proteins derived from whole human adult

CC and foetal brains and human adult hippocampus. Protein chips prepared

CC from the base sequences are useful for diagnosis of systematic diseases.

CC This sequence represents a human brain/hippocampus polypeptide used in

CC the scope of the invention.

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 179 MKYHVM 184
111111

RESULT 10

ID ADA55339
ADA55339 standard; protein; 567 AA.

AC ADA55339;

DT 20-NOV-2003 (first entry)

DE Human protein; SEQ ID 2907.

KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;

KW Gene Therapy; human; secretory protein; membrane proteins; cancer;

KW inflammatory disease; osteoporosis; neurological disease.

OS Homo sapiens.

PN EPI293569-A2.

PD 19-MAR-2003.

PF 21-MAR-2002; 2002EP-00006586.

PR 14-SEP-2001; 2001JP-00328381.

PR 24-JAN-2002; 2002US-0350435P.

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;

DR WPI; 2003-395539/38.

DR N-PSDB; ADA53700.

PT New polynucleotides encoding full-length polypeptides, e.g. secretory

PT and/or membrane proteins, useful for developing medicines for diseases in

PT which the gene is involved, or as target molecules for gene therapy.

PS Claim 14; SEQ ID NO 2907; 205pp; English.

CC The present invention relates to novel human secretory or membrane

CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-

CC ADA54071). The coding sequences are useful in the gene therapy of

CC diseases caused by abnormalities of the proteins, e.g. cancer,

CC inflammatory diseases, osteoporosis or neurological disease.

XX

XX

XX

XX

XX

XX

Query Match 100.0%; Score 34; DB 6; Length 567;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYHW 6
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Db 212 MKYHW 217
Search completed: September 29, 2005, 12:31:11
Job time : 80.6667 secs

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OM protein - protein search, using sw model
Run on: September 29, 2005, 12:15:33 ; Search time 20.6667 Seconds
(without alignments)
21.672 Million cell updates/sec

Title: US-10-774-147B-31
Perfect score: 34
Sequence: 1 MKYHW 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: +
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	331	4 US-09-344-882-6	Sequence 6, Appl1
2	31	91.2	406	3 US-09-108-020-4	Sequence 4, Appl1
3	31	91.2	406	3 US-09-108-020-42	Sequence 42, Appl1
4	31	91.2	406	4 US-09-344-882-14	Sequence 14, Appl1
5	31	91.2	406	4 US-09-685-296-4	Sequence 4, Appl1
6	31	91.2	406	4 US-09-685-296-42	Sequence 42, Appl1
7	30	88.2	212	2 US-08-477-396A-2	Sequence 2, Appl1
8	30	88.2	777	2 US-08-477-396A-4	Sequence 4, Appl1
9	30	88.2	779	1 US-08-426-627-4	Sequence 4, Appl1
10	30	88.2	779	1 US-08-426-627-24	Sequence 24, Appl1
11	30	88.2	779	4 US-09-461-912A-39	Sequence 39, Appl1

12	30	88.2	811	1	US-08-426-627-2	Sequence 2, Appl1
13	30	88.2	811	1	US-08-426-627-22	Sequence 22, Appl1
14	30	88.2	836	1	US-08-426-627-6	Sequence 6, Appl1
15	30	88.2	837	1	US-08-426-627-23	Sequence 23, Appl1
16	29	85.3	111	4	US-09-513-999C-4963	Sequence 4963, Ap
17	29	85.3	128	2	US-08-928-926A-1	Sequence 1, Appl1
18	29	85.3	128	3	US-09-212-149-1	Sequence 1, Appl1
19	29	85.3	527	4	US-09-103-331-4	Sequence 4, Appl1
20	29	85.3	527	4	US-09-631-594-55	Sequence 55, Appl1
21	28	85.3	634	4	US-09-385-219A-26	Sequence 26, Appl1
22	28	82.4	75	4	US-09-513-999C-7121	Sequence 7121, Ap
23	28	82.4	254	4	US-09-270-767-59881	Sequence 59881, A
24	28	82.4	442	4	US-09-857-716-20	Sequence 20, Appl1
25	28	82.4	444	4	US-09-248-796A-19173	Sequence 19173, A
26	28	82.4	466	4	US-09-857-716-18	Sequence 18, Appl1
27	28	82.4	586	4	US-09-270-767-44444	Sequence 44444, A
28	28	82.4	4866	4	US-09-424-783-2	Sequence 2, Appl1
29	28	82.4	4872	4	US-09-424-783-3	Sequence 3, Appl1
30	27	79.4	313	4	US-09-248-796A-18880	Sequence 18880, A
31	27	79.4	411	4	US-09-690-942-12	Sequence 12, Appl1
32	27	79.4	414	4	US-09-328-352-5504	Sequence 5504, Ap
33	27	79.4	578	4	US-09-690-942-10	Sequence 10, Appl1
34	27	79.4	582	1	US-08-261-086-4	Sequence 4, Appl1
35	27	79.4	582	1	US-08-261-086-6	Sequence 6, Appl1
36	26	76.5	63	4	US-09-248-796A-23083	Sequence 23083, A
37	26	76.5	73	4	US-09-248-796A-26927	Sequence 26927, A
38	26	76.5	124	4	US-09-732-210-1149	Sequence 1149, Ap
39	26	76.5	128	2	US-08-928-926A-3	Sequence 3, Appl1
40	26	76.5	128	2	US-08-928-926A-4	Sequence 4, Appl1
41	26	76.5	128	3	US-09-212-149-3	Sequence 3, Appl1
42	26	76.5	128	3	US-09-212-149-4	Sequence 4, Appl1
43	26	76.5	153	4	US-09-732-210-1748	Sequence 1748, Ap
44	26	76.5	183	4	US-09-902-540-13343	Sequence 13343, A
45	26	76.5	187	4	US-09-540-236-3818	Sequence 3818, Ap

Search completed: September 29, 2005, 12:42:01
Job time : 20.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:23:19 ; Search time 76.5 Seconds
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Title: US-10-774-147B-31
Perfect score: 34
Sequence: 1 MKYHVM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, AA:*

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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	34	100.0	6	16	US-10-774-147B-31 Sequence 31, Appl
2	34	100.0	109	9	US-09-764-864-1483 Sequence 1483, Ap
3	34	100.0	366	9	US-09-764-864-1060 Sequence 1060, Ap
4	34	100.0	567	15	US-10-094-749-2907 Sequence 2907, Ap
5	31	91.2	251	15	US-10-423-114-67856 Sequence 67856, A
6	31	91.2	331	9	US-09-344-882-6 Sequence 6, Appl
7	31	91.2	331	14	US-10-293-865-6 Sequence 6, Appl
8	31	91.2	376	15	US-10-423-114-49358 Sequence 49358, A
9	31	91.2	376	16	US-10-437-963-172422 Sequence 172422, A
10	31	91.2	383	16	US-10-425-115-257523 Sequence 257523, A
11	31	91.2	396	16	US-10-425-115-190117 Sequence 190117, A
12	31	91.2	398	16	US-10-767-701-45410 Sequence 45410, A
13	31	91.2	405	15	US-10-424-559-242534 Sequence 242534, A
14	31	91.2	406	9	US-09-344-882-14 Sequence 14, Appl
15	31	91.2	406	14	US-10-293-865-14 Sequence 14, Appl
16	31	91.2	406	15	US-10-425-114-54353 Sequence 54353, A
17	31	91.2	420	15	US-10-425-114-37072 Sequence 37072, A
18	31	91.2	423	16	US-10-437-963-204548 Sequence 204548, A
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20	30	88.2	51	15	US-10-424-559-205060 Sequence 205060, A
21	30	88.2	139	14	US-10-087-887-100 Sequence 100, App
22	30	88.2	151	15	US-10-052-648A-80 Sequence 80, Appl
23	30	88.2	177	9	US-09-864-761-42750 Sequence 42750, A
24	30	88.2	188	14	US-10-181-590-6 Sequence 6, Appl
25	30	88.2	188	14	US-10-087-887-18 Sequence 18, Appl
26	30	88.2	188	15	US-10-094-749-2359 Sequence 2359, Ap
27	30	88.2	188	15	US-10-052-648A-30 Sequence 30, Appl
28	30	88.2	188	15	US-10-052-648A-78 Sequence 78, Appl
29	30	88.2	188	15	US-10-052-648A-79 Sequence 79, Appl
30	30	88.2	192	9	US-09-764-864-872 Sequence 872, App
31	30	88.2	192	14	US-10-091-504-872 Sequence 872, App
32	30	88.2	192	14	US-10-103-313-547 Sequence 547, App
33	30	88.2	192	15	US-10-227-571-872 Sequence 872, App
34	30	88.2	428	16	US-10-474-792-446 Sequence 446, App
35	30	88.2	696	14	US-10-176-847-46 Sequence 46, Appl
36	30	88.2	721	17	US-10-855-588-50 Sequence 50, Appl
37	30	88.2	730	14	US-10-217-371-6 Sequence 6, Appl
38	30	88.2	749	17	US-10-855-588-48 Sequence 48, Appl
39	30	88.2	750	14	US-10-217-371-14 Sequence 14, Appl
40	30	88.2	751	14	US-10-217-371-4 Sequence 4, Appl
41	30	88.2	751	17	US-10-855-588-46 Sequence 46, Appl
42	30	88.2	751	17	US-10-936-626-121 Sequence 121, App
43	30	88.2	751	17	US-10-938-061-121 Sequence 121, App
44	30	88.2	758	14	US-10-217-371-10 Sequence 10, Appl
45	30	88.2	771	14	US-10-217-371-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-774-147B-31

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; Sequence 31, Application US/10774147B
; Publication No. US20040248255A1
; GENERAL INFORMATION:
; APPLICANT: POSTECH Foundation
; APPLICANT: POSCO
; APPLICANT: RYU, Sung-Ho
; APPLICANT: BAE, Yoo-Sik
; APPLICANT: PARK, Eun-Young
; APPLICANT: SUH, Pam-Ghill
; TITLE OF INVENTION: LEUKOCYTE STIMULATING PEPTIDES
; FILE REFERENCE: 10050-03USA
; CURRENT APPLICATION NUMBER: US/10/774,147B
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,621
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: P20
US-10-774-147B-31
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKYHVM 6

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; Sequence 1483, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1483
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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; LOCATION: (100)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1483

Query Match 100.0%; Score 34; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYHVM 6
| | | | |
Db 11 MKYHVM 16

RESULT 3

US-09-764-1060
; Sequence 1060, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1060
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1060

Query Match 100.0%; Score 34; DB 9; Length 366;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYHVM 6
| | | | |
Db 11 MKYHVM 16

RESULT 4

US-10-094-749-2907
; Sequence 2907, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAKECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, KOTOYUKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2907
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2907

Query Match 100.0%; Score 34; DB 15; Length 567;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYHVM 6
| | | | |
Db 212 MKYHVM 217

Search completed: September 29, 2005, 12:49:48
Job time : 77.5 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:13:23 ; Search time 14.5 Seconds
(without alignments)
39.814 Million cell updates/sec

Title: US-10-774-147B-31

Perfect score: 34

Sequence: 1 MKYHVM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	406	2 C66425	probable pyruvate
2	31	91.2	406	2 E84758	probable pyruvate
3	30	88.2	732	2 T19923	hypothetical prote
4	30	88.2	779	2 S36111	osteoblast-specifi
5	30	88.2	811	2 S36109	osteoblast-specifi
6	30	88.2	836	2 S36110	osteoblast-specifi
7	30	88.2	1174	2 S57060	probable membrane
8	29	85.3	61	2 C70245	hypothetical prote
9	29	85.3	243	2 H70227	antigen, P35 homol
10	29	85.3	319	2 T15463	hypothetical prote
11	29	85.3	332	2 C83933	penicillin-binding
12	29	85.3	451	2 G70241	hypothetical prote
13	29	85.3	491	2 S61715	clathrin-associate

14	29	85.3	1657	2 T25421	hypothetical prote
15	29	85.3	3110	2 AC0116	probable virulence
16	28	82.4	96	2 S78638	hypothetical prote
17	28	82.4	237	2 C82002	probable cell divi
18	28	82.4	237	2 B81230	septum site-determ
19	28	82.4	283	2 D82659	hypothetical prote
20	28	82.4	288	2 I48743	ryanodine receptor
21	28	82.4	377	2 T27805	hypothetical prote
22	28	82.4	464	2 H82011	probable outer mem
23	28	82.4	466	2 A81239	outer membrane pro
24	28	82.4	475	2 C96503	protein F9C16.7 (l
25	28	82.4	868	2 T25716	hypothetical prote
26	28	82.4	932	2 E84534	hypothetical prote
27	28	82.4	1121	2 T25715	hypothetical prote
28	28	82.4	4859	2 S74173	ryanodine receptor
29	28	82.4	4868	2 B54161	ryanodine-binding
30	28	82.4	4872	2 S27272	ryanodine receptor
31	27	79.4	92	2 A97230	hypothetical prote
32	27	79.4	141	2 F71070	hypothetical prote
33	27	79.4	148	2 T23839	hypothetical prote
34	27	79.4	242	2 F84016	hypothetical prote
35	27	79.4	247	2 F69060	conserved hypothet
36	27	79.4	486	2 T39456	zinc finger protei
37	27	79.4	566	2 F71403	hypothetical prote
38	27	79.4	570	2 A39597	phycoene dehydroge
39	27	79.4	570	2 S54134	phycoene dehydroge
40	27	79.4	582	2 S29314	phycoene dehydroge
41	27	79.4	583	2 A45381	phycoene dehydroge
42	27	79.4	620	2 T19907	hypothetical prote
43	27	79.4	664	2 B73532	cytochrome c-type
44	27	79.4	750	2 F90571	lipoprotein (impor
45	27	79.4	757	2 B90572	lipoprotein (impor

Search completed: September 29, 2005, 12:39:51
Job time : 15.5 secs

OK protein - protein search, using sw model

Run on: September 29, 2005, 12:11:58 / Search time 70 Seconds
(without alignments)
43.893 Million cell updates/sec

Title: US-10-774-147B-31

Perfect score: 34

Sequence: 1 MKYHVM 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03: +
1: uniprot_sprot: +
2: uniprot_trembl: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	204	2 Q6AXW7	Q6AXW7 rattus norv
2	34	100.0	490	2 Q86XK6	Q86XK6 homo sapien
3	34	100.0	562	2 Q8BJF3	Q8BJF3 mus musculu
4	34	100.0	565	2 Q9SJVS	Q9SJVS macaca fasc
5	34	100.0	567	1 2512 HUMAN	Q96me7 homo sapien
6	34	100.0	591	2 Q69ZS9	Q69ZS9 mus musculu
7	31	91.2	286	2 Q9FKH7	Q9FKH7 arabisidopsi
8	31	91.2	287	2 Q65087	Q65087 picea maria
9	31	91.2	406	2 Q24458	Q24458 arabisidopsi
10	31	91.2	406	2 Q64688	Q64688 arabisidopsi
11	31	91.2	406	2 Q8LAJ3	Q8LAJ3 arabisidopsi
12	31	91.2	406	2 Q9C6Z3	Q9C6Z3 arabisidopsi
13	31	91.2	457	2 Q8Y159	Q8Y159 arabisidopsi
14	31	91.2	635	2 Q82U81	Q82U81 nitrosomona
15	31	91.2	1033	2 Q6Q964	Q6Q964 oryctolagus

ALIGNMENTS

RESULT 1

ID	Q6AXW7	PRELIMINARY;	PRT;	204 AA.
AC	Q6AXW7			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Hypothetical protein.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
NCBI_TaxID=10116;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strusberg R., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhut N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			

16	31	91.2	1094	1	ATHL_RABIT	Q9V52 oryctolagus
17	31	91.2	3619	2	Q9U573	Q9U573 dictyosteli
18	30	88.2	58	2	Q7P892	Q7P892 fusobacteri
19	30	88.2	98	2	Q6PKZ1	Q6PKZ1 oryctolagus
20	30	88.2	137	2	Q8BWD7	Q8BWD7 m mus muscu
21	30	88.2	188	1	DUST1_HUMAN	Q8ne10 homo sapien
22	30	88.2	188	2	Q8VE01	Q8ve01 m dual spec
23	30	88.2	215	2	Q8HZM3	Q8hzm3 bos taurus
24	30	88.2	217	2	Q6LZU9	Q6LZU9 picropophilus
25	30	88.2	428	2	Q8BPI1	Q8BPI1 streptococc
26	30	88.2	428	2	Q9A0F6	Q9A0F6 streptococc
27	30	88.2	428	2	Q7CF94	Q7CF94 streptococc
28	30	88.2	732	2	Q27480	Q27480 caenorhabdi
29	30	88.2	810	2	Q6GUJ3	Q6guj3 mus musculu
30	30	88.2	836	1	POSN_HUMAN	Q15063 homo sapien
31	30	88.2	838	1	POSN_MOUSE	Q62009 mus musculu
32	30	88.2	936	2	Q6BH21	Q6bh21 dabryomyce
33	30	88.2	1174	1	YJLI_YEAST	P47108 saccharomyc
34	30	88.2	1869	2	Q6LF66	Q6LF66 plasmodium
35	29	85.3	61	2	Q50758	Q50758 borrelia bu
36	29	85.3	104	2	Q6BN60	Q6bn60 dabryomyce
37	29	85.3	115	2	Q7PSJ5	Q7psj5 anopheles g
38	29	85.3	120	2	Q7Y4N7	Q7y4n7 bacteriophag
39	29	85.3	127	1	NB7M_HUMAN	Q95139 homo sapien
40	29	85.3	162	2	Q8B1N8	Q8B1n8 pseudomonas
41	29	85.3	177	1	YP98_CAEEL	Q09246 caenorhabdi
42	29	85.3	243	2	Q50725	Q50725 borrelia bu
43	29	85.3	289	2	Q17846	Q17846 caenorhabdi
44	29	85.3	317	2	Q7N3M4	Q7n3m4 photorhabd
45	29	85.3	332	2	Q9KAM0	Q9kam0 bacillus ha

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC079285; AAH79285.1; -
 DR GO; GO:0008138; F:protein tyrosine/serine/threonine phosphata. . ; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR Pfam; PF00782; DSpec; 1.
 DR SMART; SM00195; DSpec; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolyase, Hypothetical protein.
 SQ SEQUENCE 204 AA; 22754 MW; 1A5BEC759522E442 CRC64;
 Query Match 100.0%; Score 34; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKYHM 6
 Db 120 MKYHM 125
 RESULT 2
 ID Q86KK6 PRELIMINARY; PRT; 490 AA.
 AC Q86KK6;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE ZNF512 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Ahtshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (Jan-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC043221; AAH43221.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00966; Zf-C2H2; 3.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2 1; 3.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2 2; 2.
 SQ SEQUENCE 490 AA; 56362 MW; E4222A04CBAD1411 CRC64;
 Query Match 100.0%; Score 34; DB 2; Length 490;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKYHM 6
 Db 135 MKYHM 140
 RESULT 3
 ID Q8BUF3 PRELIMINARY; PRT; 562 AA.
 AC Q8BUF3;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched
 DE library, clone:0230008H22 product:hypothetical zinc finger, C2H2 type
 DE containing protein, full insert sequence.
 GN Name=Zfp512;
 OS Mus musculus (Mouse).
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=12345678; PubMed=12345678; DOI=10.1073/pnas.1234567890;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RX MEDLINE=20350913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujiwaka S., Inoue K., Togawa Y., Izawa M., Onara E., Wachihi M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 Fukuda S., Furuno M., Hanegaki T., Hara A., Hashizume W.,
 Hayashida K., Hayatsu N., Hiramoto K., Hiroaka T., Hirokane T.,
 Hori F., Inotani K., Ishii Y., Itoh M., Kigawa T., Kishikawa T.,
 Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda H., Koya S.,
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK084205; BAC39137.1; -.
 DR MGI: MGI:1917345; Zfp512.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF00096; zf-C2H2; 2.
 DR SMART: SM00353; Znf_C2H2; 5.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 562 AA; 63827 MW; C75FE2A587B988 CRC64;
 Query Match 100.0%; Score 34; DB 2; Length 562;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRYHM 6
 Db 215 MKRYHM 220
 RESULT 4
 ID Q95JVS PRELIMINARY; PRT; 565 AA.
 AC Q95JVS;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 ON NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Otsuda N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
 RA Terao K., Sugeno S., Hashimoto K.;
 RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
 in the human genome sequence.";
 RL BMC Genomics 3:36-36(2002).
 DR EMBL: AB070073; BAB63018.1; -.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF00096; zf-C2H2; 3.
 DR SMART: SM00353; Znf_C2H2; 4.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Hypothetical protein.
 SO SEQUENCE 565 AA; 64495 MW; 56346681DBE038D CRC64;

Query Match 100.0%; Score 34; DB 2; Length 565;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKRYHM 6
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 Db 211 MKRYHM 216

RESULT 5
 ID 2512 HUMAN STANDARD; PRT; 567 AA.
 AC O96ME7; O96JM0;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Zinc finger protein 512.
 GN Name=ZNF512; Synonyms=KIAA1805;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed:14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Ozutsu T., Sugiyama T., Irie R.,
 Wakematsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 Naharai K., Murakami K., Yasuda T., Iwayanagi T., Magatsuma M.,
 Shihara T., Sudo H., Hosoi K., Hoshino K., Kodaiva H., Kondo H.,
 Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
 Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T.,
 Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 Imose N., Kusashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
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 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujimura T.,
 Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno Y., Yamashita R.,
 Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 RN [2]
 RP SEQUENCE OF 34-567 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21245130; PubMed=11347906;
 RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XX.
 The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro".
 RL DNA Res. 8:65-93 (2001).
 CC -1- FUNCTION: May be involved in transcriptional regulation.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: Belongs to the Krueppel C2H2-type zinc-finger protein
 family.
 CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC -----
 DR EMBL; AK057028; BAB71348.1; -.
 DR EMBL; AB058708; BAB47434.1; -.
 DR Genbank; HNC42380; ZNF512.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00966; zf-C2H2; 4.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW DNA-binding; Metal-binding; Nuclear protein; Repeat;
 KW Transcription regulation; Zinc-finger.
 FT ZN_FING 197 220 C2H2-type 1.
 FT ZN_FING 287 310 C2H2-type 2.
 FT ZN_FING 406 430 C2H2-type 3 (atypical).
 FT ZN_FING 440 463 C2H2-type 4.
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Query Match 100.0%; Score 34; DB 1; Length 567;
 Best Local Similarity 100.0%; Pred. No. 56;
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 Db 212 MKRYHM 217

RESULT 6
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 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
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 GN Name=mkIAA1805;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Embryonic intestinal tract;
 RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hirooka S.,
 RA Saga Y., Saito S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
 RA Nagase T., Ohara O., Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
 RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
 RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
 RT Randomly Sampled from Size-Fractionated Libraries.";
 RL DNA Res. 11:205-218(2004).
 DR EMBL; AK173267; BAD3245.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; ZF-C2H2; 2.
 DR SMART; SM00353; ZNF_C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 2.
 FT NON TER 1
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Search completed: September 29, 2005, 12:38:17
 Job time : 70 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:04:53 ; Search time 80.6667 Seconds
(without alignments)
28.767 Million cell updates/sec

Title: US-10-774-147B-32
Perfect score: 34
Sequence: 1 MKYK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: geneseq_16dec04: +
2: geneseq_1980s: +
3: geneseq_1990s: +
4: geneseq_2000s: +
5: geneseq_2001s: +
6: geneseq_2002s: +
7: geneseq_2003s: +
8: geneseq_2004s: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	30	88.2	2435	ABB60448	Abb60448 Drosophi1
5	29	85.3	6	ADR44739	Adr44739 Human leu
6	29	85.3	6	ADR44745	Adr44745 Human leu
7	29	85.3	6	ADR44749	Adr44749 Human leu
8	29	85.3	45	AAI14039	Aai14039 Repeat se
9	29	85.3	46	ABR83863	ABr83863 Bacillus

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11	29	85.3	80	5	ADH32511	Adh32511 Yeast smo
12	29	85.3	220	2	AAV31800	Aav31800 Beak and
13	29	85.3	361	8	ADK16799	Adk16799 Nemoarcha
14	29	85.3	397	2	AAW04217	Aaw04217 Rat dorsta
15	29	85.3	397	2	AAW76437	Aaw76437 Human p53
16	29	85.3	397	2	AAV06512	Aav06512 Human P2X
17	29	85.3	397	3	AAE29597	Aae29597 Human P2X
18	29	85.3	397	3	AAE29598	Aae29598 Rat P2X-3
19	29	85.3	397	4	AAE01140	Aae01140 Rat purin
20	29	85.3	397	4	AAE01139	Aae01139 Human pur
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24	29	85.3	432	2	AAV08219	Aav08219 Staphyloc
25	29	85.3	469	8	ADP99149	Adp99149 Human tra
26	29	85.3	584	8	ADS24442	Ads24442 Bacteria1
27	29	85.3	844	8	AD141017	Ad141017 Goldfish
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33	28	82.4	70	8	ADL04940	Adl04940 M. catarr
34	28	82.4	110	3	ABA44118	Ab44118 Human can
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36	28	82.4	328	8	ABM84451	Abm84451 Human dia
37	28	82.4	359	8	ADL90227	Adl90227 Human enz
38	28	82.4	371	8	ABM84450	Abm84450 Human dia
39	28	82.4	372	6	ABU54644	Abu54644 Human NOV
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42	28	82.4	390	7	ADD44985	Add44985 Rat Prote
43	28	82.4	390	7	ADD44987	Add44987 Human Pro
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ALIGNMENTS

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DT	04-NOV-2004 (first entry)
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DE	Human leukocyte stimulating peptide, P21.
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KW	Archidonic acid release; AA release; intracellular calcium release;
KW	acquired immune deficiency syndrome; infectious disease;
KW	leukocyte stimulating peptide; human.
OS	Homo sapiens.

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14	28	82.4	390	4	US-09-685-296-36	Sequence 36, App1
15	28	82.4	397	4	US-09-901-151-2	Sequence 2, App1
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17	28	82.4	562	4	US-09-902-540-11161	Sequence 11161, A
18	27	79.4	78	4	US-09-732-210-351	Sequence 351, App
19	27	79.4	80	4	US-09-732-210-342	Sequence 342, App1
20	27	79.4	80	4	US-09-732-210-344	Sequence 344, App
21	27	79.4	80	4	US-09-732-210-343	Sequence 343, App
22	27	79.4	80	4	US-09-732-210-353	Sequence 353, App
23	27	79.4	80	4	US-09-834-133-32	Sequence 32, App1
24	27	79.4	93	4	US-09-732-210-339	Sequence 339, App
25	27	79.4	93	4	US-09-732-210-340	Sequence 340, App
26	27	79.4	127	4	US-09-270-767-42359	Sequence 42359, A
27	27	79.4	156	2	US-09-070-060-7	Sequence 7, App11
28	27	79.4	156	3	US-09-051-969A-3	Sequence 3, App11
29	27	79.4	156	3	US-09-051-969A-4	Sequence 4, App11
30	27	79.4	156	3	US-09-357-746-7	Sequence 7, App11
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33	27	79.4	229	4	US-09-248-796A-19846	Sequence 19846, A
34	27	79.4	360	4	US-09-501-115-4	Sequence 4, App11
35	27	79.4	2987	2	US-08-970-269A-29	Sequence 29, App1
36	27	79.4	2987	3	US-09-407-562-29	Sequence 29, App1
37	27	79.4	3959	2	US-08-970-269A-30	Sequence 30, App1
38	27	79.4	3959	3	US-09-407-562-30	Sequence 30, App1
39	26	76.5	8	5	PCT-US95-02140-1	Sequence 1, App11
40	26	76.5	29	3	US-08-433-522A-41	Sequence 41, App1
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42	26	76.5	29	3	US-08-942-046-41	Sequence 41, App1
43	26	76.5	78	4	US-09-732-210-341	Sequence 341, App
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Search completed: September 29, 2005, 12:42:02
Job time : 21.6667 secs

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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:23:19 ; Search time 76.5 Seconds
(without alignments)
32.558 Million cell updates/sec

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Perfect score: 34
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	29	85.3	45	18	US-10-654-637-104	Sequence 104, App
8	29	85.3	46	14	US-10-321-897-155	Sequence 155, App
9	29	85.3	46	14	US-10-318-673-155	Sequence 155, App
10	29	85.3	80	14	US-10-083-357-969	Sequence 969, App
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13	29	85.3	349	17	US-10-732-923-22783	Sequence 22783, A
14	29	85.3	349	17	US-10-732-923-22784	Sequence 22784, A
15	29	85.3	397	16	US-10-817-607-7	Sequence 7, Appl
16	29	85.3	398	15	US-10-282-122A-51625	Sequence 51625, A
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18	29	85.3	415	18	US-10-703-649-49	Sequence 49, Appl
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22	29	85.3	844	15	US-10-436-715-33	Sequence 33, Appl
23	29	85.3	844	15	US-10-436-715-77	Sequence 77, Appl
24	29	85.3	849	16	US-10-437-963-171250	Sequence 171250,
25	29	85.3	1228	15	US-10-282-122A-71769	Sequence 71769, A
26	29	85.3	1573	16	US-10-437-963-179356	Sequence 179356,
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32	28	82.4	372	15	US-10-114-270-206	Sequence 206, App
33	28	82.4	388	18	US-10-972-963-70	Sequence 70, Appl
34	28	82.4	390	9	US-09-901-151-5	Sequence 5, Appl
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44	28	82.4	414	9	US-09-901-151-4	Sequence 4, Appl
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ALIGNMENTS

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; Sequence 32, Application US/10774147B
; Publication No. US20040248255A1
; GENERAL INFORMATION:
; APPLICANT: POSTECH Foundation
; APPLICANT: POSCO
; APPLICANT: RYU, Sung-Ho
; APPLICANT: BAE, Yoo-Sik
; APPLICANT: PARK, Eun-Young
; APPLICANT: SUH, Pann-Ghill
; TITLE OF INVENTION: LEUKOCYTE STIMULATING PEPTIDES
; FILE REFERENCE: 10050-03USA
; CURRENT APPLICATION NUMBER: US/10/774,147B
; PRIORITY FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,621
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
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; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: P21
US-10-774-147B-32
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
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Job time : 76.5 secs
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RESULT 1
US-10-774-147B-32

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:13:23 / Search time 14.5 Seconds
(without alignments)
39,814 Million cell updates/sec

Title: US-10-774-147B-32

Perfect score: 34

Sequence: 1 MKYRM 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 28346 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: +
1: p1r1: +
2: p1r2: +
3: p1r3: +
4: p1r4: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	515	2 B90324	hypothetical prote
2	31	91.2	5825	2 T12117	polypeptin - fava
3	30	88.2	579	2 H88632	protein F56B3.7 [1
4	30	88.2	969	2 S17909	hypothetical prote
5	30	88.2	1197	2 S26947	DNA-directed DNA p
6	30	88.2	1245	2 D71613	GAF domain protein
7	29	85.3	133	2 B97270	CBS domain contain
8	29	85.3	201	2 T26272	ORF MSV111 hypothe
9	29	85.3	202	2 S11434	proteinase - bovin
10	29	85.3	240	2 H69932	hypothetical prote
11	29	85.3	391	2 G90253	formate hydrogenly
12	29	85.3	397	2 S60334	putinoceptor P2X -
13	29	85.3	397	2 I58099	gene P2X3 protein

14	29	85.3	398	2 B97341	glycosyltransferas
15	29	85.3	401	2 T48576	protein kinase-lik
16	29	85.3	545	2 B88479	protein F47D12.9 (
17	29	85.3	608	2 T06632	hypothetical prote
18	29	85.3	745	2 T23893	hypothetical prote
19	29	85.3	1232	2 S40766	hypothetical prote
20	29	85.3	2295	2 B71621	probable membrane
21	28	82.4	290	2 C75190	cobalamin biosynth
22	28	82.4	314	2 A11123	B. subtilis YqfA p
23	28	82.4	314	2 AC1484	B. subtilis YqfA p
24	28	82.4	388	1 DEHUP7	pyruvate dehydroge
25	28	82.4	389	1 DEHUP7	pyruvate dehydroge
26	28	82.4	390	1 DEHUP7	pyruvate dehydroge
27	28	82.4	390	1 DEHUP7	pyruvate dehydroge
28	28	82.4	390	1 DEHUP7	pyruvate dehydroge
29	28	82.4	390	2 S23506	pyruvate dehydroge
30	28	82.4	477	2 AC1923	site-specific DNA-
31	28	82.4	525	2 F96674	Flt616.8 (imported
32	28	82.4	538	2 E81435	probable iron-upta
33	28	82.4	1077	2 A97306	superfamily II DNA
34	27	79.4	32	2 B40186	ubiquitin / riboso
35	27	79.4	81	2 A49103	sequence-specific
36	27	79.4	132	2 F69596	mercuric resistanc
37	27	79.4	149	1 UONCR	ubiquitin / riboso
38	27	79.4	150	2 T39081	ubiquitin-like pro
39	27	79.4	154	2 T46664	ubiquitin/S27a fus
40	27	79.4	155	2 H90774	hypothetical prote
41	27	79.4	156	1 I52328	ubiquitin / riboso
42	27	79.4	156	1 UQHUR7	ubiquitin / riboso
43	27	79.4	156	1 UQFRF7	ubiquitin / riboso
44	27	79.4	163	2 B48766	ubiquitin-like pro
45	27	79.4	163	2 A48766	ubiquitin / riboso

Search completed: September 29, 2005, 12:39:51
Job time : 14.5 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:11:58 ; Search time 70 Seconds
(without alignments)
43.893 Million cell updates/sec

Title: US-10-774-147B-32

Perfect score: 34

Sequence: 1 MKYYKM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	72	2 Q6EB84	Q6EB84 campylobact
2	31	91.2	37	2 Q6RXY5	Q6RXY5 bacillus an
3	31	91.2	37	2 Q6F013	Q6F013 bacillus an
4	31	91.2	37	2 Q74NM2	Q74NM2 bacillus ce
5	31	91.2	129	2 Q7Y3Q4	Q7Y3Q4 enterobacte
6	31	91.2	170	2 Q7RC52	Q7RC52 plasmidium
7	31	91.2	377	2 Q6FKN1	Q6FKN1 candida gla
8	31	91.2	515	2 Q97X53	Q97X53 sulfolobus
9	31	91.2	5825	2 Q6B731	Q6B731 vitia faba
10	30	88.2	42	2 Q6HE15	Q6HE15 varroa dest
11	30	88.2	127	2 Q91W79	Q91W79 arachidopis
12	30	88.2	180	2 Q832U8	Q832U8 enterococu
13	30	88.2	391	2 Q7VQ02	Q7VQ02 candidatus
14	30	88.2	465	2 Q6GUC6	Q6GUC6 edwardsiell
15	30	88.2	541	2 Q45109	Q45109 caenorhabdi

16	30	88.2	793	2 Q6H92	Q6H92 dictyostell
17	30	88.2	969	1 DPOM_NEUIN	P33538 neurospora
18	30	88.2	1245	2 Q96195	Q96195 plasmidium
19	30	88.2	2893	2 Q9M433	Q9M433 drosophila
20	29	85.3	51	2 Q6V790	Q6V790 campococcus
21	29	85.3	51	2 Q6V790	Q6V790 campococcus
22	29	85.3	110	2 Q91AB7	Q91AB7 brachydanio
23	29	85.3	120	2 Q91AB8	Q91AB8 brachydanio
24	29	85.3	133	2 Q97EUB	Q97EUB clostridium
25	29	85.3	146	2 Q6M652	Q6M652 bovine aden
26	29	85.3	184	2 Q6KXK6	Q6KXK6 beak and fe
27	29	85.3	184	2 Q6KXK7	Q6KXK7 beak and fe
28	29	85.3	184	2 Q6KXK8	Q6KXK8 beak and fe
29	29	85.3	184	2 Q6KXK9	Q6KXK9 beak and fe
30	29	85.3	184	2 Q6KXK0	Q6KXK0 beak and fe
31	29	85.3	184	2 Q6KXK1	Q6KXK1 beak and fe
32	29	85.3	184	2 Q6KXK2	Q6KXK2 beak and fe
33	29	85.3	199	2 Q70AP2	Q70AP2 beak and fe
34	29	85.3	201	2 Q9YVY1	Q9YVY1 melanoplus
35	29	85.3	202	1 ADEN_ADEB7	P19151 bovine aden
36	29	85.3	204	2 Q8XJ77	Q8XJ77 clostridium
37	29	85.3	235	2 Q7PD30	Q7PD30 anopheles g
38	29	85.3	240	1 YPBE_BKCSU	P50731 bacillus su
39	29	85.3	239	2 Q6SHZ7	Q6SHZ7 bacillus su
40	29	85.3	288	2 Q6BSX2	Q6BSX2 beak and fe
41	29	85.3	288	2 Q6BSX3	Q6BSX3 beak and fe
42	29	85.3	288	2 Q6A1G4	Q6A1G4 beak and fe
43	29	85.3	289	2 Q6BSY0	Q6BSY0 beak and fe
44	29	85.3	289	2 Q6BSY2	Q6BSY2 beak and fe
45	29	85.3	289	2 Q6BSY4	Q6BSY4 beak and fe

ALIGNMENTS

RESULT 1

ID	Q6EB84	PRELIMINARY;	PRT;	72 AA.
AC	Q6EB84;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Tgn045 (Fragment).			
OS	Campylobacter jejuni.			
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;			
OC	Campylobacteriaceae; Campylobacter.			
OX	NCBI_TaxID=197;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TGH 9011;			
RX	PubMed=15231810; DOI=10.1128/JB.186.14.4781-4795.2004;			
RA	Poly F., Threadgill D., Stintzi A.;			
RT	"Identification of Campylobacter jejuni ATCC 43431-Specific Genes by			
RT	Whole Microbial Genome Comparisons."			
RL	J. Bacteriol. 186:4781-4795(2004).			
DR	EMBL; AY501934; AAS99001.1; -.			
FT	NON_TER	72	72	

50 SEQUENCE 72 AA; 8601 MW; 7488655C2DC04630 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 72;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKYYKM 6
|||||

Db 1 MKYYKM 6

Search completed: September 29, 2005, 12:38:17

Job time : 70 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:04:53 ; Search time 80.6667 Seconds
(without alignments)
28.767 Million cell updates/sec

Title: US-10-774-1478-33

Perfect score: 36

Sequences: 1 MKYPM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003s:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	ADR44752	Adt44752 Human Ieu
2	33	91.7	262	ADP98662	Adm98662 Geranylge
3	33	91.7	262	ADP98632	Adm98632 Geranylge
4	33	91.7	262	ADN17402	Adn17402 Bacterial
5	32	88.9	593	ADS43852	Ads43852 Bacterial
6	31	86.1	6	ADR44746	Adt44746 Human Ieu
7	31	86.1	6	ADR44740	Adt44740 Human Ieu
8	31	86.1	141	AAW28103	AAW28103 Amino aci
9	31	86.1	330	AAW63590	AAW63590 Staphyloc

10	31	86.1	330	AAW59996	AAW59996 Cell divi
11	31	86.1	425	AAV43639	AAV43639 Amino aci
12	31	86.1	425	ADJ50217	Adj50217 Oil-asease
13	31	86.1	435	ADS41859	Ads41859 Bacterial
14	31	86.1	439	AAW59995	AAW59995 Cell divi
15	31	86.1	439	AAU36756	AAU36756 Staphyloc
16	31	86.1	439	AAU33979	AAU33979 Staphyloc
17	31	86.1	439	ABU15917	Abu15917 Protein e
18	31	86.1	440	ABM71279	Abm71279 Staphyloc
19	31	86.1	1194	ABU24346	Abu24346 Protein e
20	30	83.3	260	AAW03520	AAW03520 Balli reat
21	30	83.3	435	ADN24236	Adn24236 Bacterial
22	29	80.6	60	ADF70002	Adf70002 AcmaA-type
23	29	80.6	107	AD051596	Ad051596 Human TAG
24	29	80.6	170	ADD27658	Add27658 Human acti
25	29	80.6	171	ADD27389	Add27389 Human acti
26	29	80.6	212	ADR08078	Adr08078 Human pro
27	29	80.6	224	ABR54023	AbR54023 Lactococc
28	29	80.6	224	ADS29330	Ads29330 Bacterial
29	29	80.6	227	ABU40124	Abu40124 Protein e
30	29	80.6	228	ABU41513	Abu41513 Protein e
31	29	80.6	232	AAU33655	AAU33655 Pseudomon
32	29	80.6	232	ABU15506	Abu15506 Protein e
33	29	80.6	245	ABO77745	AbO77745 Pseudomon
34	29	80.6	250	ADG36926	Adg36926 A. pernix
35	29	80.6	250	AD119379	Ad119379 Aeropyrum
36	29	80.6	250	ADS44522	Ads44522 Bacterial
37	29	80.6	327	ADN20106	Adn20106 Bacterial
38	29	80.6	347	ADN23670	Adn23670 Bacterial
39	29	80.6	445	AKG52882	AKG52882 S. epider
40	29	80.6	454	ABP39593	Abp39593 Staphyloc
41	29	80.6	454	AD505587	Ad505587 Staphyloc
42	29	80.6	457	ABM72660	Abm72660 Staphyloc
43	29	80.6	478	ADN23912	Adn23912 Bacterial
44	29	80.6	495	ADN23982	Adn23982 Bacterial
45	29	80.6	510	AAW88360	AAW88360 Caenorhab

ALIGNMENTS

RESULT 1	ADR44752	standard; peptide; 6 AA.
ID	ADR44752	
XX	AC	ADR44752:
XX	DT	04-NOV-2004 (first entry)
XX	DE	Human leukocyte stimulating peptide, P22.
XX	KW	Arachidonic acid release; AA release; intracellular calcium release;
KW	KW	immune response; pathogen; infectious disease;
KW	KW	acquired immune deficiency syndrome; AIDS; cancer; gene therapy;
KW	KW	leukocyte stimulating peptide; human.
XX	OS	Homo sapiens.

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:15:33 ; Search time 20.6667 Seconds
(without alignments)
21.672 Million cell updates/sec

Title: US-10-774-147B-33
Perfect score: 36
Sequence: 1 MKYYPM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:++
1: /cgn2_6/prodata/1/laa/5A_CONB.p:ep:++
2: /cgn2_6/prodata/1/laa/5B_CONB.p:ep:++
3: /cgn2_6/prodata/1/laa/6A_CONB.p:ep:++
4: /cgn2_6/prodata/1/laa/6B_CONB.p:ep:++
5: /cgn2_6/prodata/1/laa/PCtUS_CONB.p:ep:++
6: /cgn2_6/prodata/1/laa/backfiles1.p:ep:++

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	31	86.1	330	2 US-08-827-615-2	Sequence 2, App11
2	31	86.1	330	3 US-08-921-209-4	Sequence 4, App11
3	31	86.1	330	3 US-09-411-763-4	Sequence 4, App11
4	31	86.1	425	4 US-09-293-549-6	Sequence 6, App11
5	31	86.1	439	3 US-08-921-209-2	Sequence 2, App11
6	31	86.1	439	3 US-09-411-763-2	Sequence 2, App11
7	31	86.1	526	1 US-08-399-986B-4	Sequence 4, App11
8	31	86.1	526	2 US-08-493-754A-4	Sequence 4, App11
9	30	83.3	260	1 US-08-595-559-1	Sequence 1, App11
10	29	80.6	245	4 US-09-252-991A-26491	Sequence 26491, A
11	29	80.6	445	4 US-09-710-279-2858	Sequence 2858, Ap

XX Key Location/Qualifiers
FH Modified-site 6
FT /note="C-terminal amide"
FT

XX WO2004069858-A2.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004WO-KR000225.

XX 07-FEB-2003; 2003US-0455621P.

XX (POSC-) POSCO.

XX (POST-) POSTECH FOUND.

XX Ryu S, Bae Y, Park E, Suh P;

XX WPI; 2004-604410/58.

XX New leukocyte stimulating polypeptides useful for stimulating arachidonic acid release in target cells or for causing intracellular calcium

XX release, and in gene therapy applications, such as to enhance immune response to bacteria.

XX Claim 1; SEQ ID NO 33; 57pp; English.

XX The present invention relates to a target cell stimulating peptide where the target cell may be a leukocyte or a phagocyte. The invention is useful for stimulating arachidonic acid (AA) and intracellular calcium release in human leukocytic cells and for superoxide generation in human neutrophils. The invention is also used to enhance immune response to pathogens such as bacteria and viruses and in the treatment of infectious diseases such as acquired immune deficiency syndrome (AIDS) and cancer. The invention is also useful in gene therapy. The present sequence is human leukocyte stimulating peptide. This sequence is used in the invention.

XX Sequence 6 AA;

XX Query Match 100.0%; Score 36; DB 8; Length 6;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 MKYYPM 6

XX DB 1 MKYYPM 6

XX Search completed: September 29, 2005, 12:31:12

XX Job time : 80.6667 secs

12	29	80.6	454	3	US-09-134-001C-4438	Sequence 4438, Ap
13	29	80.6	510	1	US-08-249-112-3	Sequence 3, Appl1
14	29	80.6	510	5	PCT-US95-0656-3	Sequence 23, Appl1
15	29	80.6	515	3	US-08-369-822C-23	Sequence 38, Appl1
16	29	80.6	515	3	US-08-582-776C-38	Sequence 35, Appl1
17	29	80.6	515	3	US-08-434-831B-35	Sequence 3812, Ap
18	29	77.8	90	4	US-09-328-352-5812	Sequence 3914, Ap
19	28	77.8	109	3	US-09-134-001C-3914	Sequence 76, Appl1
20	28	77.8	151	4	US-09-861-451A-76	Sequence 1, Appl1
21	28	77.8	171	2	US-08-946-528-3	Sequence 15959, A
22	28	77.8	200	3	US-09-519-729-1	Sequence 34689, A
23	28	77.8	207	4	US-09-248-796A-19595	Sequence 49906, A
24	28	77.8	241	4	US-09-270-767-34689	Sequence 5840, Ap
25	28	77.8	241	4	US-09-270-767-49906	Sequence 4737, Ap
26	28	77.8	248	4	US-09-134-000C-5840	Sequence 8907, Ap
27	28	77.8	250	4	US-09-107-532A-4737	Sequence 4219, Ap
28	28	77.8	250	4	US-09-489-039A-8907	Sequence 40258, A
29	28	77.8	274	4	US-09-134-000C-4219	Sequence 6431, Ap
30	28	77.8	284	4	US-09-270-767-40258	Sequence 55474, A
31	28	77.8	284	4	US-09-270-767-55474	Sequence 6365, Ap
32	28	77.8	295	4	US-09-543-681A-6431	Sequence 12692, A
33	28	77.8	296	4	US-09-107-532A-6365	Sequence 60873, A
34	28	77.8	394	4	US-09-949-016-7566	Sequence 18130, A
35	28	77.8	413	4	US-09-489-039A-12692	Sequence 43800, A
36	28	77.8	464	4	US-09-270-767-60873	Sequence 14652, A
37	28	77.8	485	4	US-09-248-796A-18130	Sequence 16770, A
38	28	77.8	505	4	US-09-270-767-43800	Sequence 19292, A
39	28	77.8	517	4	US-09-248-796A-14652	Sequence 8841, Ap
40	28	77.8	539	4	US-09-248-796A-16770	Sequence 8842, Ap
41	28	77.8	609	4	US-09-248-796A-19292	Sequence 2, Appl1
42	28	77.8	654	4	US-09-949-016-8841	Sequence 11277, A
43	28	77.8	654	4	US-09-949-016-8842	
44	28	77.8	743	3	US-09-077-354B-2	
45	28	77.8	773	4	US-09-949-016-11277	

Search completed: September 29, 2005, 12:42:02
Job time : 20.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:23:19 ; Search time 76.5 Seconds
(without alignments)
32.558 Million cell updates/sec

Title: US-10-774-147B-33
Perfect score: 36
Sequence: 1 MKRYPM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues
Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
 - 5: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
 - 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
 - 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
 - 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
 - 17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pep:*
 - 18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
 - 19: /cgn2_6/ptodata/1/pubppaa/US11A_PUBCOMB.pep:*
 - 20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
 - 21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
 - 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	100.0	6	16	US-10-774-147B-33	Sequence 33, Appl
2	33	91.7	262	15	US-10-369-493-55	Sequence 55, Appl
3	33	91.7	262	15	US-10-041-018-52	Sequence 52, Appl
4	33	91.7	262	15	US-10-041-018-82	Sequence 82, Appl
5	32	88.9	593	15	US-10-369-493-22282	Sequence 22282, A
6	32	88.9	593	17	US-10-732-923-2014	Sequence 2014, Ap
7	31	86.1	6	16	US-10-774-147B-21	Sequence 21, Appl
8	31	86.1	6	16	US-10-774-147B-27	Sequence 27, Appl
9	31	86.1	73	15	US-10-424-599-155735	Sequence 155735,
10	31	86.1	149	15	US-10-425-114-42384	Sequence 42384, A
11	31	86.1	149	16	US-10-425-115-219414	Sequence 219414,
12	31	86.1	335	13	US-10-062-254-356	Sequence 356, App
13	31	86.1	383	17	US-10-732-923-22885	Sequence 22885, A
14	31	86.1	396	17	US-10-732-923-22887	Sequence 22887, A
15	31	86.1	406	13	US-10-062-254-332	Sequence 332, App
16	31	86.1	425	15	US-10-389-566-2221	Sequence 2221, Ap
17	31	86.1	435	15	US-10-369-493-20289	Sequence 20289, A
18	31	86.1	439	9	US-09-815-242-5475	Sequence 5475, Ap
19	31	86.1	439	9	US-09-815-242-12349	Sequence 12349, A
20	31	86.1	439	15	US-10-282-122A-43841	Sequence 43841, A
21	31	86.1	609	17	US-10-732-923-22866	Sequence 334, App
22	31	86.1	613	13	US-10-062-294-334	Sequence 179249,
23	31	86.1	613	16	US-10-437-963-179249	Sequence 22885, A
24	31	86.1	615	17	US-10-732-923-22863	Sequence 22863, A
25	31	86.1	617	17	US-10-425-114-63811	Sequence 63811, A
26	31	86.1	634	15	US-10-425-114-63785	Sequence 63785, A
27	31	86.1	750	16	US-10-437-963-179251	Sequence 179251,
28	31	86.1	1194	15	US-10-282-122A-52270	Sequence 52270, A
29	31	86.1	70	15	US-10-424-599-198903	Sequence 198903,
30	30	83.3	188	16	US-10-425-115-341266	Sequence 341266,
31	30	83.3	435	15	US-10-369-493-6889	Sequence 6889, Ap
32	29	80.6	70	16	US-10-425-115-359868	Sequence 359868,
33	29	80.6	224	15	US-10-369-493-18363	Sequence 18363, A
34	29	80.6	227	15	US-10-282-122A-68048	Sequence 68048, A
35	29	80.6	228	15	US-10-282-122A-69437	Sequence 69437, A
36	29	80.6	232	9	US-09-815-242-5151	Sequence 5151, Ap
37	29	80.6	232	15	US-10-282-122A-43430	Sequence 43430, A
38	29	80.6	250	15	US-10-369-493-22952	Sequence 22952, A
39	29	80.6	250	15	US-10-316-233-6	Sequence 6, Appl
40	29	80.6	250	17	US-10-732-923-21411	Sequence 21411, A
41	29	80.6	327	15	US-11-084-394-6	Sequence 6, Appl
42	29	80.6	347	15	US-10-369-493-6323	Sequence 6323, Ap
43	29	80.6	347	15	US-10-369-493-6323	Sequence 6323, Ap
44	29	80.6	454	18	US-10-724-972A-4882	Sequence 4882, Ap
45	29	80.6				

Search completed: September 29, 2005, 12:49:48
Job time : 76.5 secs

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OM protein - protein search, using sw model
Run on: September 29, 2005, 12:13:23 ; Search time 14.5 Seconds
(without alignments)
39.814 Million cell updates/sec

Title: US-10-774-147B-33
Perfect score: 36
Sequence: 1 MKYYPM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_79:++
1: pirl:++
2: pirl2:++
3: pirl3:++
4: pirl4:++

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	91.7	262	2	E70365	geranylgeranyl pyr
2	33	91.7	574	2	C86400	hypothetical prote
3	32	88.9	348	2	T19885	hypothetical prote
4	32	88.9	593	2	S38145	uoporphyrinogen m
5	31	86.1	193	2	D72367	hypothetical prote
6	31	86.1	220	2	T33592	hypothetical prote
7	31	86.1	425	1	S48469	probable membrane
8	31	86.1	439	2	C89890	hypothetical prote
9	31	86.1	466	2	H71234	probable 4-aminobu
10	31	86.1	557	2	E72282	oligopeptide ABC t
11	31	86.1	562	2	C72278	hypothetical prote
12	31	86.1	976	2	E75212	oligosaccharyl tra
13	31	86.1	1308	2	T15280	hypothetical prote

14	31	86.1	1444	1	A43377	RNA-directed RNA p
15	30	83.3	260	2	S71507	restriction endonu
16	30	83.3	435	2	T19840	hypothetical prote
17	29	80.6	224	2	F86713	hypothetical prote
18	29	80.6	232	2	C81139	outer membrane pro
19	29	80.6	250	2	B72454	probable thiorox
20	29	80.6	258	2	F69515	hypothetical prote
21	29	80.6	327	1	S76143	probable aldehyde
22	29	80.6	347	2	T29742	hypothetical prote
23	29	80.6	348	2	B97720	hypothetical prote
24	29	80.6	414	2	T22539	hypothetical prote
25	29	80.6	457	2	D90057	hypothetical prote
26	29	80.6	461	2	S30864	avermectin-sensiti
27	29	80.6	478	2	T24805	hypothetical prote
28	29	80.6	495	2	T20754	hypothetical prote
29	29	80.6	583	2	E83794	ABC transporter (A
30	29	80.6	1146	2	S07915	RF2 protein - yeast
31	29	80.6	2116	1	ZLWNSY	genome polypeptide
32	28	77.8	140	2	D27577	T-cell receptor al
33	28	77.8	141	2	S21647	T-cell receptor al
34	28	77.8	146	2	S21646	T-cell receptor al
35	28	77.8	147	2	S21648	T-cell receptor al
36	28	77.8	151	2	G90036	hypothetical prote
37	28	77.8	164	2	S48422	hypothetical prote
38	28	77.8	200	2	B75137	ubiquitinone/menaqu
39	28	77.8	201	2	H90025	molyscenum transpo
40	28	77.8	210	2	T48879	proteasome psmb, b
41	28	77.8	218	2	G71722	probable glutamine
42	28	77.8	246	2	AF1057	hypothetical prote
43	28	77.8	253	2	A88955	protein K04F1.1 (f
44	28	77.8	255	2	T00725	hypothetical prote
45	28	77.8	302	2	A61193	creatine kinase (E

Search completed: September 29, 2005, 12:39:51
Job time : 14.5 secs

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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:11:58 ; Search time 70 Seconds

(without alignments)
43.893 Million cell updates/sec

Title: US-10-774-147B-33

Perfect score: 36

Sequence: 1 MKYVPM 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	% Match	Length	DB ID	Description
1	33	91.7	262	1	ISPA_XOLNE	066952 aquifex aeo
2	33	91.7	273	2	Q6CHE9	06che9 yarrowia li
3	33	91.7	574	2	Q9SXC9	09sxc9 arabidopsis
4	32	88.9	145	2	Q6SFT0	06sft0 uncultured
5	32	88.9	237	2	Q8SBC3	08sbc3 dasyhelea s
6	32	88.9	364	2	O17659	017659 caenorhabdi
7	32	88.9	524	2	O8UJ22	08uj22 carcopi thec
8	32	88.9	593	1	SUMT_YEAST	P36150 saccharomyc
9	31	86.1	193	2	Q9WZ04	09wz04 thermotoga
10	31	86.1	210	2	Q974J1	0974j1 sulfolobus
11	31	86.1	214	2	Q7RFU7	07rfu7 plasmodium
12	31	86.1	220	2	Q9TZAG	09tza6 caenorhabdi
13	31	86.1	259	2	Q6E0T8	06e0t8 borrelia he
14	31	86.1	273	2	Q6C124	06c124 yarrowia li
15	31	86.1	335	2	O07671	007671 enterococcu

16	31	86.1	422	2	Q6CLC9	Q6c1c9 kluyveromyc
17	31	86.1	425	1	YIK3_YEAST	P40487 saccharomyc
18	31	86.1	426	2	Q75A29	Q75az9 ashyva gosa
19	31	86.1	439	2	Q07324	Q07324 staphylococ
20	31	86.1	439	2	Q8NX34	Q8nx34 staphylococ
21	31	86.1	439	2	Q99UT0	Q99ut0 staphylococ
22	31	86.1	439	2	Q7A618	Q7a618 staphylococ
23	31	86.1	440	2	Q6GA28	Q6ga28 staphylococ
24	31	86.1	440	2	Q6GHQ1	Q6ghq1 staphylococ
25	31	86.1	466	2	Q57878	Q57878 pyrococcus
26	31	86.1	517	2	Q7R3P5	Q7r3p5 giardia lam
27	31	86.1	557	2	Q9X0V0	Q9x0v0 thermotoga
28	31	86.1	562	2	Q9X0V3	Q9x0v3 thermotoga
29	31	86.1	613	2	Q65X38	Q65x38 oryza sativ
30	31	86.1	615	2	Q62162	Q62162 burkholderi
31	31	86.1	615	2	Q63RF7	Q63rf7 burkholderi
32	31	86.1	699	2	Q7U5M5	Q7u5m5 synechococc
33	31	86.1	811	2	Q6TW71	Q6tw71 orf virus.
34	31	86.1	959	2	Q7QNT4	Q7qnt4 giardia lam
35	31	86.1	976	2	Q9V250	Q9v250 pyrococcus
36	31	86.1	1262	2	Q7XNL1	Q7xnl1 oryza sativ
37	31	86.1	1308	2	Q01924	Q01924 caenorhabdi
38	31	86.1	1444	1	RRPL_RDVA	RRPL_RDVA
39	31	86.1	1444	1	RRPL_RDVF	RRPL_RDVF
40	30	83.3	170	2	Q6P4V6	Q6p4v6 brachydanio
41	30	83.3	193	2	Q7RN94	Q7rn94 plasmodium
42	30	83.3	260	2	P71102	P71102 cutibacter
43	30	83.3	303	2	Q64W36	Q64w36 bacteroides
44	30	83.3	460	2	Q18518	Q18518 caenorhabdi
45	30	83.3	460	2	Q7RKB3	Q7rbk3 plasmodium

Search completed: September 29, 2005, 12:38:17
Job time : 70 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:04:53 ; Search time 80.6667 Seconds
(without alignments)
28.767 Million cell updates/sec

Title: US-10-774-147B-34

Perfect score: 33

Sequence: 1 MKYYVM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: geneseq_16Dec04:*
- 2: geneseq_1980s:*
- 3: geneseq_1990s:*
- 4: geneseq_2000s:*
- 5: geneseq_2001s:*
- 6: geneseq_2002s:*
- 7: geneseq_2003as:*
- 8: geneseq_2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	6	ADR44753	Adr44753 Human leu
2	30	90.9	121	ABM72061	Abm72061 Staphyloc
3	29	87.9	457	ABP27386	Abp27386 Streptoco
4	29	87.9	462	ABU44132	Abu44132 Protein e
5	29	87.9	483	ABP27387	Abp27387 Streptoco
6	29	87.9	483	ABU46597	Abu46597 Protein e
7	28	84.8	6	ADR44741	Adr44741 Human leu
8	28	84.8	6	ADR44750	Adr44750 Human leu
9	28	84.8	6	ADR44754	Adr44754 Human leu

10	28	84.8	6	ADR44747	Adr44747 Human leu
11	28	84.8	109	AAU16530	Aau16530 Human nov
12	28	84.8	109	ABU55599	Abu55599 Human nov
13	28	84.8	263	ABU20742	Abu20742 Protein e
14	28	84.8	280	ABBS9912	Abbs9912 Human mac
15	28	84.8	320	ABU23721	Abu23721 Protein e
16	28	84.8	366	AAU16107	Aau16107 Human nov
17	28	84.8	366	ABU51176	Abu51176 Human nov
18	28	84.8	408	ABBS1479	Abbs1479 Drosophi1
19	28	84.8	408	AAE10837	Aae10837 Drosophi1
20	28	84.8	482	ADR39740	Adr39740 Human kin
21	28	84.8	490	ABE99649	Abpe99649 Human pol
22	28	84.8	490	AAO16430	Aao16430 Human nuc
23	28	84.8	534	ADG42180	Adg42180 Human bra
24	28	84.8	557	AAW4997	Aaw4997 YAK-1 rel
25	28	84.8	566	ABMS4614	Abms4614 Human dia
26	28	84.8	567	ADA55339	Adas55339 Human pro
27	28	84.8	584	ADB85519	Adbs85519 Human knb
28	28	84.8	629	AAW93441	Aaw93441 Human pro
29	28	84.8	629	ADL31049	Adl31049 Human pro
30	28	84.8	629	ABM82107	Abm82107 Tumour-as
31	28	84.8	635	AAW9262	Aaw9262 Human pro
32	28	84.8	676	AAW80246	Aaw80246 Human pro
33	28	84.8	763	AAW41734	Aaw41734 Human TRA
34	28	84.8	763	AAU02222	Aau02222 Rat DyfK,
35	28	84.8	763	AAU02221	Aau02221 Human knb
36	28	84.8	763	ABBS1155	Abbs1155 Mouse lac
37	28	84.8	763	ABBS4250	Abbs4250 Human NOV
38	28	84.8	1048	AAK44506	Aak44506 Balamv coa
39	28	84.8	1202	AAK44507	Aak44507 Balamv coa
40	28	84.8	1456	AAK49042	Aak49042 NKDA rece
41	28	84.8	1480	AAU77228	Aau77228 Human NR2
42	28	84.8	1482	AAK44193	Aak44193 Rat NKDA
43	28	84.8	1482	AAK45944	Aak45944 Glutamic
44	28	84.8	1482	ADG62166	Adg62166 Rat Proce
45	28	84.8	1482	ADG99951	Adg99951 Rat NR2B

ALIGNMENTS

RESULT 1
ID ADR44753 standard; peptide; 6 AA.
XX
AC ADR44753:
XX
DT 04-NOV-2004 (first entry)

XX Human leukocyte stimulating peptide, P23.
DE Arachidonic acid release; AA release; intracellular calcium release;
XX Acquired immune response; pathogen; infectious disease;
KW immune response; pathogen; infectious disease;
KW acquired immune deficiency syndrome; AIDS; cancer; gene therapy;
KW leukocyte stimulating peptide; human.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH Modified-site 6
FT /note="C-terminal amide"
XX
XX WO2004069858-A2.
XX
XX 19-AUG-2004.
XX
XX 06-FEB-2004; 2004WO-KR000225.
XX
XX 07-FEB-2003; 2003US-0455621P.
XX
XX (POSC-) POSCO.
XX (POST-) POSTECH FOUNO.
XX
XX Ryu S, Bae Y, Park E, Suh P;
XX
XX WPI; 2004-604410/58.
XX
XX New leukocyte stimulating polypeptides useful for stimulating arachidonic
PT acid release in target cells or for causing intracellular calcium
PT release, and in gene therapy applications, such as to enhance immune
PT response to bacteria.
XX
XX Claim 1; SEQ ID NO 34; 57pp; English.
XX
XX The present invention relates to a target cell stimulating peptide where
CC the target cell may be a leukocyte or a phagocyte. The invention is
CC useful for stimulating arachidonic acid (AA) and intracellular calcium
CC release in human leukocytic cells and for superoxide generation in human
CC neutrophils. The invention is also used to enhance immune response to
CC pathogens such as bacteria and viruses and in the treatment of infectious
CC diseases such as acquired immune deficiency syndrome (AIDS) and cancer.
CC The invention is also useful in gene therapy. The present sequence is
CC human leukocyte stimulating peptide. This sequence is used in the
CC invention.
XX
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 33; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKRYVM 6
| | | | |
DB 1 MKRYVM 6
Search completed: September 29, 2005, 12:31:12
Job time : 80.6667 secs

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OM protein - protein search, using sw model
Run on: September 29, 2005, 12:15:33 ; Search time 20.6667 Seconds
(without alignments)
21.672 Million cell updates/sec
Title: US-10-774-147B-34
Perfect score: 33
Sequence: 1 MKRYVM 6
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 513545 seqs, 7464964 residues
Total number of hits satisfying chosen parameters: 513545
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued Patents_AA: +
1: /cgn2_6/ptodata/1/laa/5A.COMB.pep: +
2: /cgn2_6/ptodata/1/laa/5B.COMB.pep: +
3: /cgn2_6/ptodata/1/laa/6A.COMB.pep: +
4: /cgn2_6/ptodata/1/laa/6B.COMB.pep: +
5: /cgn2_6/ptodata/1/laa/PCtus.COMB.pep: +
6: /cgn2_6/ptodata/1/laa/backfiles1.pep: +
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result Query
No. Score Match Length DB ID Description

1 30 90.9 310 4 US-09-248-796A-17322 Sequence 17322, A
2 28 84.8 408 4 US-09-802-213-9 Sequence 9, Appl1
3 28 84.8 557 3 US-09-027-064-2 Sequence 2, Appl1
4 28 84.8 557 3 US-09-271-815-2 Sequence 2, Appl1
5 28 84.8 763 2 US-08-677-862-2 Sequence 2, Appl1
6 28 84.8 763 2 US-09-252-571-2 Sequence 2, Appl1
7 28 84.8 763 3 US-09-434-065-2 Sequence 2, Appl1
8 28 84.8 763 3 US-08-789-275-4 Sequence 4, Appl1
9 28 84.8 763 3 US-08-789-275-4 Sequence 4, Appl1
10 28 1063 4 US-09-270-767-44682 Sequence 5, Appl1
11 28 84.8 1347 4 US-09-949-016-9603 Sequence 9603, Ap

12	28	84.8	1456	1	US-08-026-138E-8	Sequence 8, Appli
13	28	84.8	1482	1	US-08-026-138E-2	Sequence 2, Appli
14	28	84.8	1484	2	US-08-231-193A-56	Sequence 56, Appl
15	28	84.8	1484	2	US-08-486-273A-56	Sequence 56, Appl
16	28	84.8	1484	3	US-08-940-035A-56	Sequence 56, Appl
17	28	84.8	1484	3	US-08-940-035A-56	Sequence 56, Appl
18	28	84.8	1484	3	US-08-935-105A-56	Sequence 56, Appl
19	28	84.8	1484	3	US-08-264-578-2	Sequence 56, Appl
20	28	84.8	1484	4	US-09-648-797-56	Sequence 56, Appl
21	28	84.8	1484	4	US-09-386-123-56	Sequence 56, Appl
22	28	84.8	1484	4	US-09-949-016-5998	Sequence 56, Appl
23	28	84.8	1484	4	US-10-038-937-56	Sequence 56, Appl
24	27	81.8	73	4	US-09-489-039A-8297	Sequence 8297, Ap
25	27	81.8	106	4	US-09-543-681A-7810	Sequence 7810, Ap
26	27	81.8	227	4	US-09-270-767-48713	Sequence 48713, A
27	27	81.8	228	4	US-09-270-767-33496	Sequence 33496, A
28	27	81.8	320	3	US-09-463-702A-41	Sequence 41, Appl
29	27	81.8	320	4	US-09-699-135-41	Sequence 41, Appl
30	27	81.8	327	4	US-09-543-681A-8331	Sequence 8331, Ap
31	27	81.8	393	2	US-08-559-303B-74	Sequence 74, Appl
32	27	81.8	393	3	US-09-175-828-74	Sequence 74, Appl
33	27	81.8	393	4	US-09-753-143-74	Sequence 74, Appl
34	27	81.8	403	4	US-09-802-213-5	Sequence 5, Appl
35	27	81.8	414	4	US-09-802-213-3	Sequence 3, Appl
36	27	81.8	424	4	US-09-248-796A-2123	Sequence 2123, A
37	27	81.8	488	4	US-09-248-796A-18644	Sequence 18644, A
38	27	81.8	580	3	US-08-913-159-10	Sequence 10, Appl
39	27	81.8	594	2	US-08-910-856-2	Sequence 2, Appl
40	27	81.8	639	4	US-09-270-767-61294	Sequence 61294, A
41	27	81.8	764	4	US-09-270-767-45772	Sequence 45772, A
42	27	81.8	1122	4	US-09-489-039A-8554	Sequence 8554, Ap
43	27	81.8	1417	2	US-08-559-303B-78	Sequence 78, Appl
44	27	81.8	1417	3	US-08-781-891-78	Sequence 78, Appl
45	27	81.8	1417	3	US-09-175-828-78	Sequence 78, Appl

Search completed: September 29, 2005, 12:42:02
Job time : 20.6667 secs

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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:23:19 ; Search time 76.5 Seconds
(without alignments)
32,558 Million cell updates/sec

Title: US-10-774-147B-34
Perfect score: 33
Sequence: 1 MKYVM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 segs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB	ID
1	33	100.0	6	16 US-10-774-147B-34
2	29	87.9	28	15 US-10-424-599-206986
3	29	87.9	462	15 US-10-282-122A-72056
4	29	87.9	483	15 US-10-282-122A-74621
5	29	87.9	1229	16 US-10-437-963-13817
6	29	87.9	1407	16 US-10-437-963-13720
7	28	84.8	6	16 US-10-774-147B-22
8	28	84.8	6	16 US-10-774-147B-28
9	28	84.8	6	16 US-10-774-147B-31
10	28	84.8	6	16 US-10-774-147B-35
11	28	84.8	13	18 US-10-948-707-1092
12	28	84.8	109	9 US-09-764-864-1483
13	28	84.8	122	16 US-10-425-115-271499
14	28	84.8	237	16 US-10-437-963-193233
15	28	84.8	263	15 US-10-282-122A-48666
16	28	84.8	264	16 US-10-425-115-256190
17	28	84.8	320	15 US-10-282-122A-51645
18	28	84.8	366	9 US-09-764-864-1060
19	28	84.8	408	9 US-09-802-213-9
20	28	84.8	408	16 US-10-625-492-9
21	28	84.8	408	20 US-11-097-143-11229
22	28	84.8	421	16 US-10-664-421-132
23	28	84.8	421	18 US-10-941-635-134
24	28	84.8	491	14 US-10-156-761-12739
25	28	84.8	531	10 US-09-922-011-11
26	28	84.8	567	15 US-10-094-749-2907
27	28	84.8	671	16 US-10-425-115-264832
28	28	84.8	763	15 US-10-236-417-168
29	28	84.8	1480	10 US-09-922-011-10
30	28	84.8	1484	9 US-09-945-901-56
31	28	84.8	1484	13 US-10-007-747-56
32	28	84.8	1484	14 US-10-038-937-56
33	28	84.8	1484	14 US-10-146-806-2
34	28	84.8	1829	17 US-10-732-923-22633
35	27	81.8	6	16 US-10-774-147B-32
36	27	81.8	6	16 US-10-774-147B-33
37	27	81.8	24	15 US-10-424-599-276251
38	27	81.8	121	15 US-10-424-599-218487
39	27	81.8	167	16 US-10-501-282-4760
40	27	81.8	194	16 US-10-767-701-61959
41	27	81.8	219	18 US-10-501-282-4762
42	27	81.8	255	18 US-10-501-282-4764
43	27	81.8	258	18 US-10-501-282-4766
44	27	81.8	259	18 US-10-994-726-607
45	27	81.8	287	18 US-10-450-763-48011

ALIGNMENTS

```

; Sequence 34, Application US/10774147B
; Publication No. US20040248255A1
; GENERAL INFORMATION:
; APPLICANT: POSTECH Foundation
; APPLICANT: POSCO
; APPLICANT: RYU, Sung-Ho
; APPLICANT: BAE, Yoo-Sik
; APPLICANT: PARK, Eun-Young
; APPLICANT: SUH, Penn-Gh11
; TITLE OF INVENTION: LEUKOCYTE STIMULATING PEPTIDES
; FILE REFERENCE: 10050-03USA
; CURRENT APPLICATION NUMBER: US/10774,147B
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,621
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: P23
US-10-774-147B-34

```

```

Query Match 100.0%; Score 33; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKRYM 6
DB 1 MKRYM 6
Search completed: September 29, 2005, 12:49:48
Job time : 76.5 secs

```

RESULT 1
US-10-774-147B-34

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:13:23 ; Search time 14.5 Seconds
(without alignments)
39,814 Million cell updates/sec

Title: US-10-774-147B-34

Perfect score: 33

Sequence: 1 MKYYVM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_79:*

2: PIR1:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	30	90.9	1010	2	B86259
2	30	90.9	1036	2	A42895
3	29	87.9	196	2	B96980
4	28	84.8	53	2	S42286
5	28	84.8	73	2	AE2594
6	28	84.8	84	2	C90210
7	28	84.8	111	1	WOBP67
8	28	84.8	277	1	G71101
9	28	84.8	320	2	C97206
10	28	84.8	335	2	E71201
11	28	84.8	366	2	E90525
12	28	84.8	471	2	A45616
13	28	84.8	589	2	JG0196

14	28	84.8	629	2	JG0195	protein kinase DYR
15	28	84.8	727	2	JC7818	metalloprotease
16	28	84.8	754	2	JC4898	Down-syndrome-crit
17	28	84.8	757	2	E97230	trehalose/maltose
18	28	84.8	1041	2	PQ0442	polyprotein - barl
19	28	84.8	1202	2	PQ0440	polyprotein - barl
20	28	84.8	1482	2	I49704	glutamate receptor
21	28	84.8	1482	2	B43274	N-methyl-D-asparta
22	28	84.8	1484	2	S52086	genome polyprotein
23	28	84.8	2652	1	VFIHB2	hypothetical prote
24	28	84.8	3498	2	T22330	hypothetical prote
25	27	81.8	129	2	E90331	D-allulose-6-phosp
26	27	81.8	231	2	D65217	probable integral
27	27	81.8	307	2	A71605	rod shape-determi
28	27	81.8	337	2	D69660	cell-shape determi
29	27	81.8	337	2	AD1268	cell-shape determi
30	27	81.8	337	2	AE1630	cell-shape determi
31	27	81.8	345	1	MFVNSY	matrix protein - S
32	27	81.8	404	2	A44833	lactococci (EC 3.4
33	27	81.8	457	2	T19109	hypothetical prote
34	27	81.8	459	2	T19110	hypothetical prote
35	27	81.8	460	2	T19111	hypothetical prote
36	27	81.8	465	2	T19113	hypothetical prote
37	27	81.8	469	2	T34173	hypothetical prote
38	27	81.8	505	2	T28276	hypothetical prote
39	27	81.8	522	2	T28113	ORF MSV15 probabl
40	27	81.8	688	2	S50580	hypothetical prote
41	27	81.8	1107	2	B91271	probable periplasm
42	27	81.8	1107	2	B86112	probable periplasm
43	27	81.8	1107	2	E65226	hypothetical 123.8
44	27	81.8	1108	2	AE1047	probable membrane
45	27	81.8	1417	2	A57570	Bloom's syndrome r

Search completed: September 29, 2005, 12:39:31
Job time : 14.5 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:11:58 ; Search time 70 Seconds

(without alignments)
43.893 Million cell updates/sec

Title: US-10-774-147B-34

Perfect score: 33

Sequence: 1 MKYYVM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	335	2	Q8GP65	Q8GP65 streptococc
2	32	97.0	373	2	Q697F8	Q697F8 neomaskellii
3	30	90.9	108	2	Q8BJN3	Q8BJN3 shewanelia
4	30	90.9	226	2	Q9QW05	Q9QW05 rattus sp.
5	30	90.9	287	2	Q8V3Q3	Q8V3Q3 swinepox vi
6	30	90.9	490	2	Q621P8	Q621P8 burkholderi
7	30	90.9	490	2	Q63VM0	Q63VM0 burkholderi
8	30	90.9	1010	2	Q91N91	Q91N91 arabidopsis
9	30	90.9	1035	1	ATHL_MOUSE	Q921W8 mus musculu
10	30	90.9	1036	1	ATHL_RAT	P94708 rattus norv
11	30	90.9	1163	2	Q8XKW3	Q8XKW3 clostridium
12	30	90.9	1574	2	Q6DRCT	Q6DRCT brachydanio
13	29	87.9	187	2	Q64T61	Q64T61 bacteroides
14	29	87.9	196	2	Q97LE0	Q97LE0 clostridium
15	29	87.9	364	1	TRU2_THETN	Q8T7F0 thermomaer

ALIGNMENTS

16	29	87.9	417	2	Q6CMW6	Q6CMW6 kluyveromyc
17	29	87.9	457	2	Q8E0T8	Q8E0T8 streptococc
18	29	87.9	457	2	Q8E6F6	Q8E6F6 streptococc
19	29	87.9	462	2	Q8DUV5	Q8DUV5 streptococc
20	29	87.9	483	2	Q8K721	Q8K721 streptococc
21	29	87.9	483	2	Q8P0H3	Q8P0H3 streptococc
22	29	87.9	483	2	Q99285	Q99285 streptococc
23	29	87.9	483	2	Q878W3	Q878W3 streptococc
24	29	87.9	588	2	Q6N209	Q6N209 rhodospseud
25	29	87.9	597	2	Q6ZEB8	Q6ZEB8 burkholderi
26	29	87.9	597	2	Q63IW2	Q63IW2 burkholderi
27	29	87.9	613	2	Q89HC1	Q89HC1 bredyrhizob
28	29	87.9	633	2	Q8MTK1	Q8MTK1 meloidogyne
29	29	87.9	817	2	Q7OAN0	Q7QAN0 anopheles g
30	29	87.9	1806	2	Q6LFB1	Q6LFB1 plasmodium
31	29	87.9	3290	2	Q7RRX0	Q7RRX0 plasmodium
32	28	84.8	53	2	Q6WY58	Q6WY58 bacterioph
33	28	84.8	53	2	Q6WYR9	Q6WYR9 bacterioph
34	28	84.8	73	2	Q8U127	Q8U127 agrobacteri
35	28	84.8	84	2	Q97ZQ8	Q97ZQ8 sulfolobus
36	28	84.8	103	2	Q6Y7K6	Q6Y7K6 streptilococ
37	28	84.8	105	2	Q8D9S2	Q8D9S2 vibrio vuln
38	28	84.8	111	1	V06_BP77	P03778 bacterioph
39	28	84.8	117	2	Q6T7A8	Q6T7A8 candida gla
40	28	84.8	123	2	Q9PW83	Q9PW83 myxocephal
41	28	84.8	129	2	Q8XNC3	Q8XNC3 clostridium
42	28	84.8	164	2	Q8X052	Q8X052 neurospora
43	28	84.8	187	2	Q812B8	Q812B8 plasmodium
44	28	84.8	204	2	Q6XKW7	Q6XKW7 rattus norv
45	28	84.8	226	2	Q8U107	Q8U107 brachydanio

RESULT 1

Q8GP65	ID	Q8GP65	PRELIMINARY;	PRT;	335 AA.
AC	Q8GP65;	01-MAR-2003 (TREMblrel. 23, Created)			
DT	01-MAR-2003 (TREMblrel. 23, Last sequence update)				
DT	01-JUN-2003 (TREMblrel. 24, Last annotation update)				
DE	Eps100.				
GN	Name=eps100;				
OS	Streptococcus thermophilus.				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OX	NCBI_TaxID=1308;				
RN	SEQUENCE FROM N.A.				
RP	Rallu F., Ehrlich D.S., Renault P.;				
RA	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
RL	EMBL: AF454500; AN63775.1; -				
DR	CO; GO:0016741; F:transferase activity, transferring groups o. . . ; IEA.				
DR	InterPro: IPR002656; Acyl_transf_3.				
DR	Pfam: PF01757; Acyl_transf_3; 1.				
DR	SEQUENCE 335 AA; 39165 MW; 3DA218614060BC92 CRC64;				

Query Match 100.0%; Score 33; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKYYVM 6
111111
Db 200 MKYYVM 205
Search completed: September 29, 2005, 12:38:18
Job time : 71 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:04:53 ; Search time 80.6667 Seconds
(without alignments)
28.767 Million cell updates/sec

Title: US-10-774-147B-35

Perfect score: 36

Sequence: 1 MKYYM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp190s:*
- 3: geneseqp200s:*
- 4: geneseqp201s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	ADR44754	Adr44754 Human leu
2	33	91.7	477	ABB64297	Abb64297 Drosophila
3	33	91.7	482	AAK72601	AAK72601 Truncated
4	33	91.7	484	ABB6961	Abb6961 Drosophila
5	33	91.7	504	AAK24482	AAK24482 Cholesterol
6	33	91.7	504	AAK72507	AAK72507 Human chl
7	33	91.7	504	AAK73945	AAK73945 Human cho
8	33	91.7	504	ABB9292	Abb9292 Human cyp
9	33	91.7	504	ABP57063	Abp57063 Human cyp

10	33	91.7	504	7	ADD48632	Add48632 Human Pro
11	33	91.7	504	7	ADF90913	Adf90913 Human hsp
12	33	91.7	504	8	ADI19748	Adi19748 Human cyp
13	31	86.1	6	8	ADR44742	Adr44742 Human leu
14	31	86.1	6	8	ADR44748	Adr44748 Human leu
15	31	86.1	91	5	ABP42120	Abp42120 Human leu
16	31	86.1	110	4	AAU40774	AAU40774 Human ova
17	31	86.1	110	6	ABM37293	Abm37293 Proteolomb
18	31	86.1	148	5	ABP38990	Abp38990 Staphyloc
19	31	86.1	148	8	ADS06816	Ads06816 Staphyloc
20	31	86.1	169	3	AAK47284	Aak47284 Arabidops
21	31	86.1	169	3	AAK11709	Aak11709 Arabidops
22	31	86.1	215	4	ABB65782	Abb65782 Drosophila
23	31	86.1	276	3	AAK11708	Aak11708 Arabidops
24	31	86.1	297	5	AAU73401	AAU73401 Ethlichia
25	31	86.1	333	3	AAK47283	Aak47283 Arabidops
26	31	86.1	406	2	AAK12395	Aak12395 Transcrip
27	31	86.1	432	6	ADB10724	Adb10724 Alloloccoc
28	31	86.1	434	6	ABP75890	Abp75890 Human sec
29	31	86.1	438	6	ADB10722	Adb10722 Alloloccoc
30	31	86.1	456	6	ADB10720	Adb10720 Alloloccoc
31	31	86.1	509	2	AAK14138	Aak14138 Zea mays
32	31	86.1	509	3	AAK44603	Aak44603 Maize MRO
33	30	83.3	150	2	AAK98204	Aak98204 H. pylori
34	30	83.3	467	7	ABO61273	AbO61273 Klebsiell
35	30	83.3	845	4	ABB63110	Abb63110 Drosophila
36	29	80.6	85	4	AAK64443	Aak64443 Human Pol
37	29	80.6	89	4	AAK90587	Aak90587 Human imm
38	29	80.6	110	4	AAK01396	Aak01396 Human pol
39	29	80.6	138	2	AAK44013	Aak44013 Human tes
40	29	80.6	166	5	ABP39434	Abp39434 Staphyloc
41	29	80.6	166	8	ADS04576	AdS04576 Staphyloc
42	29	80.6	178	7	ADJ38055	Adj38055 Mortierel
43	29	80.6	178	8	ADH80142	Adh80142 Mortierel
44	29	80.6	199	7	ADF74794	Adf74794 Human NOV
45	29	80.6	203	7	ADF74792	Adf74792 Human NOV

ALIGNMENTS

RESULT 1	
ID	ADR44754 standard; peptide; 6 AA.
XX	
AC	ADR44754;
XX	
DT	04-NOV-2004 (first entry)
XX	
DE	Human leukocyte stimulating peptide, P24.
XX	
KW	Arachidonic acid release; AA release; intracellular calcium release;
KW	immune response; pathogen; infectious disease;
KW	acquired immune deficiency syndrome; AIDS; cancer; gene therapy;
KW	leukocyte stimulating peptide; human.
OS	Homo sapiens.

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model
Run on:      September 29, 2005, 12:15:33 ; Search time 20.6667 Seconds
              (without alignments)
              21.672 Million cell updates/sec

Title:      US-10-774-147B-35
Perfect score: 36
Sequence:    1 MKRYYM 6

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:    513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :      Issued_Patents_AA:*
               1: /cgn2_6/prodata/1/1aa/5A_CONKB.pep:*
               2: /cgn2_6/prodata/1/1aa/5B_CONKB.pep:*
               3: /cgn2_6/prodata/1/1aa/6A_CONKB.pep:*
               4: /cgn2_6/prodata/1/1aa/6B_CONKB.pep:*
               5: /cgn2_6/prodata/1/1aa/CTDUS_CONKB.pep:*
               6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

      #
Result No.      Score      Query Match Length DB ID      Description
-----
1      33      91.7      482      1      US-08-135-510-5      Sequence 5, Appl11
2      33      91.7      482      1      US-08-483-852-5      Sequence 5, Appl11
3      33      91.7      482      1      US-08-477-953-5      Sequence 5, Appl11
4      33      91.7      482      2      US-08-477-952-5      Sequence 5, Appl11
5      33      91.7      504      1      US-08-135-511-28      Sequence 28, Appl14
6      33      91.7      504      1      US-08-483-852-8      Sequence 8, Appl14
7      33      91.7      504      1      US-08-361-458-3      Sequence 3, Appl11
8      33      91.7      504      1      US-08-477-953-8      Sequence 8, Appl11
9      33      91.7      504      1      US-08-477-953-8      Sequence 28, Appl11
10     33      91.7      504      2      US-08-477-952-8      Sequence 8, Appl11
11     33      91.7      504      4      US-09-762-415-4      Sequence 4, Appl11

```

12	33	91.7	506	2	US-08-845-161A-18	Sequence 18, Appl
13	33	91.7	506	3	US-09-270-751-18	Sequence 18, Appl
14	33	91.7	507	4	US-09-949-016-10802	Sequence 10802, A
15	31	86.1	121	4	US-09-248-796A-14633	Sequence 14633, A
16	31	86.1	148	3	US-09-134-001C-3835	Sequence 3835, Ap
17	31	86.1	509	1	US-10-095-946-8	Sequence 8, Appl1
18	31	86.1	509	3	US-09-183-959-8	Sequence 8, Appl1
19	31	86.1	509	4	US-09-347-650-6	Sequence 6, Appl1
20	31	86.1	509	4	US-09-535-315-8	Sequence 8, Appl1
21	30	83.3	282	4	US-09-248-796A-25927	Sequence 25927, A
22	30	83.3	467	4	US-09-489-039A-7790	Sequence 7790, Ap
23	29	80.6	23	4	US-09-270-767-35352	Sequence 35352, A
24	29	80.6	23	4	US-09-270-767-50769	Sequence 50769, A
25	29	80.6	66	4	US-09-248-796A-23669	Sequence 23669, A
26	29	80.6	138	2	US-07-857-224B-112	Sequence 112, App
27	29	80.6	151	1	US-08-614-935-28	Sequence 28, Appl
28	29	80.6	151	3	US-09-130-287-28	Sequence 28, Appl
29	29	80.6	166	3	US-09-134-001C-4279	Sequence 4279, Ap
30	29	80.6	178	4	US-09-145-828A-24	Sequence 24, Appl
31	29	80.6	178	4	US-09-903-456-26	Sequence 26, Appl
32	29	80.6	219	4	US-09-903-456-38	Sequence 38, Appl
33	29	80.6	243	4	US-09-541-759-7	Sequence 7, Appl1
34	29	80.6	257	4	US-09-949-016-7490	Sequence 7490, Ap
35	29	80.6	258	4	US-09-698-781-3	Sequence 3, Appl1
36	29	80.6	259	4	US-09-270-767-57599	Sequence 37599, A
37	29	80.6	259	4	US-09-270-767-52816	Sequence 52816, A
38	29	80.6	280	4	US-09-145-828A-21	Sequence 21, Appl
39	29	80.6	280	4	US-09-903-456-28	Sequence 28, Appl
40	29	80.6	286	4	US-09-903-456-59	Sequence 59, Appl
41	29	80.6	288	4	US-09-145-828A-17	Sequence 17, Appl
42	29	80.6	289	4	US-09-903-456-21	Sequence 21, Appl
43	29	80.6	289	4	US-09-903-456-34	Sequence 34, Appl
44	29	80.6	291	4	US-09-903-456-36	Sequence 36, Appl
45	29	80.6	293	4	US-09-145-828A-12	Sequence 12, Appl

Search completed: September 29, 2005, 12:42:02
Job time : 20.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2005, 12:23:19 ; Search time 76.5 Seconds
(without alignments)
32.558 Million cell updates/sec

Title: US-10-774-147B-35
Perfect score: 36
Sequence: 1 MKYYVM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US10H_PUBCOMB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US10I_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US10J_PUBCOMB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US10K_PUBCOMB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US10L_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	100.0	6	16	US-10-774-147B-35	Sequence 35, Appl
2	33	91.7	477	20	US-11-097-143-19683	Sequence 19683, A
3	33	91.7	484	20	US-11-097-143-27675	Sequence 27675, A
4	33	91.7	504	15	US-10-186-288-6	Sequence 6, Appl
5	33	91.7	506	14	US-10-373-877-18	Sequence 18, Appl
6	31	86.1	6	16	US-10-774-147B-23	Sequence 23, Appl
7	31	86.1	6	16	US-10-774-147B-29	Sequence 29, Appl
8	31	86.1	64	15	US-10-424-599-202465	Sequence 202465, A
9	31	86.1	70	15	US-10-425-114-39473	Sequence 39473, A
10	31	86.1	71	16	US-10-425-115-282993	Sequence 282993, A
11	31	86.1	91	15	US-10-264-049-3252	Sequence 3252, Ap
12	31	86.1	130	16	US-10-425-115-189387	Sequence 189387, A
13	31	86.1	148	18	US-10-724-972A-6111	Sequence 6111, Ap
14	31	86.1	215	20	US-11-097-143-24138	Sequence 24138, A
15	31	86.1	297	9	US-09-846-808-2	Sequence 2, Appl
16	31	86.1	297	14	US-10-284-986-2	Sequence 2, Appl
17	31	86.1	297	14	US-10-369-293-2	Sequence 2, Appl
18	31	86.1	297	14	US-10-285-042-2	Sequence 2, Appl
19	31	86.1	432	18	US-10-501-282-4336	Sequence 4336, Ap
20	31	86.1	438	18	US-10-501-282-4338	Sequence 4338, Ap
21	31	86.1	456	18	US-10-501-282-4340	Sequence 4340, Ap
22	31	86.1	758	10	US-09-892-635A-34	Sequence 34, Appl
23	30	83.3	83	16	US-10-425-115-251813	Sequence 251813, A
24	30	83.3	104	16	US-10-425-115-248086	Sequence 248086, A
25	30	83.3	150	9	US-09-881-752A-8	Sequence 8, Appl
26	30	83.3	150	15	US-10-335-977-8327	Sequence 8327, Ap
27	30	83.3	154	16	US-10-767-701-52335	Sequence 52335, A
28	30	83.3	155	15	US-10-335-977-8328	Sequence 8328, Ap
29	30	83.3	264	16	US-10-425-115-274002	Sequence 274002, A
30	30	83.3	275	15	US-10-425-114-70915	Sequence 70915, A
31	30	83.3	293	16	US-10-425-115-274000	Sequence 274000, A
32	30	83.3	319	15	US-10-425-114-45060	Sequence 45060, A
33	30	83.3	324	16	US-10-425-115-238830	Sequence 238830, A
34	30	83.3	428	16	US-10-437-963-136348	Sequence 136348, A
35	30	83.3	845	20	US-11-097-143-16722	Sequence 16722, A
36	29	80.6	60	16	US-10-437-963-163220	Sequence 163220, A
37	29	80.6	84	15	US-10-424-599-226081	Sequence 226081, A
38	29	80.6	117	15	US-10-424-599-180100	Sequence 180100, A
39	29	80.6	166	18	US-10-724-972A-3871	Sequence 3871, Ap
40	29	80.6	170	16	US-10-437-963-177053	Sequence 177053, A
41	29	80.6	174	14	US-10-017-161-1688	Sequence 1688, Ap
42	29	80.6	178	9	US-09-903-456-26	Sequence 26, Appl
43	29	80.6	178	14	US-10-156-911-26	Sequence 26, Appl
44	29	80.6	178	14	US-10-408-736-23	Sequence 23, Appl
45	29	80.6	178	17	US-10-912-446-26	Sequence 26, Appl

ALIGNMENTS

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; Sequence 35, Application US/10774147B
; Publication No. US20040248255A1
; GENERAL INFORMATION:
; APPLICANT: POSTECH Foundation
; APPLICANT: POSCO
; APPLICANT: RTU, Sung-Ho
; APPLICANT: BAE, Yoo-Sik
; APPLICANT: PARK, Eun-Young
; APPLICANT: SUH, Pam-Ghill
; TITLE OF INVENTION: LEUCOCYTE STIMULATING PEPTIDES
; FILE REFERENCE: 10050-03US
; CURRENT APPLICATION NUMBER: US/10/774,147B
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,621
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: P24
US-10-774-147B-35
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Query Match 100.0%; Score 36; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MKRYM 6
Db 1 MKRYM 6

Search completed: September 29, 2005, 12:49:48
Job time : 76.5 secs
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RESULT 1
US-10-774-147B-35

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:13:23 ; Search time 14.5 Seconds
(without alignments)
39,814 Million cell updates/sec

Title: US-10-774-147B-35

Perfect score: 36

Sequence: 1 MKYYM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28346 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	91.7	416	2 T23383	hypothetical prote
2	33	91.7	501	2 I46701	cholesterol 7alpha
3	33	91.7	504	1 JH0659	cholesterol 7alpha
4	31	86.1	108	2 T17826	hypothetical prote
5	31	86.1	165	2 B97354	hypothetical prote
6	31	86.1	214	2 E46681	glutathione transf
7	31	86.1	399	2 C96908	(fs) similar to AB
8	31	86.1	406	2 A36706	transcription acti
9	31	86.1	591	1 NUZOF	glucose-6-phosphat
10	31	86.1	804	2 A37473	probable RNA polym
11	30	83.3	150	2 E64599	hypothetical prote
12	30	83.3	150	2 B71912	hypothetical prote
13	30	83.3	416	2 A70393	hypothetical prote

14	29	80.6	243	2 B33329	cysteine-rich secr
15	29	80.6	245	2 S68691	neutrophil granule
16	29	80.6	379	2 S74601	hypothetical prote
17	29	80.6	503	2 A54779	cholesterol 7alpha
18	29	80.6	504	2 S39399	cholesterol 7alpha
19	29	80.6	599	2 AD3017	hypothetical prote
20	29	80.6	599	2 D98267	ABC transporter AT
21	28	77.8	40	2 S26797	Ig heavy chain V r
22	28	77.8	81	2 A24522	mitochondrial prot
23	28	77.8	89	2 T15018	hypothetical prote
24	28	77.8	107	2 A61753	Orf19 (bacterioph
25	28	77.8	118	2 H90457	hypothetical prote
26	28	77.8	120	2 S36306	T-cell receptor de
27	28	77.8	131	2 G69442	transcription regu
28	28	77.8	161	2 H58932	ribosomal protein
29	28	77.8	164	2 H64329	hypothetical prote
30	28	77.8	182	2 T16519	hypothetical prote
31	28	77.8	194	2 A5756	pheromone biosynth
32	28	77.8	210	2 H97149	hypothetical prote
33	28	77.8	211	2 AB3178	glutathione S-tran
34	28	77.8	239	2 B84257	hypothetical prote
35	28	77.8	300	2 JC7115	ets homologous fac
36	28	77.8	300	2 JW0048	ets transcription
37	28	77.8	321	2 H45774	odorant receptor 3
38	28	77.8	321	2 H69482	hypothetical prote
39	28	77.8	359	2 C69369	hypothetical prote
40	28	77.8	359	2 T21840	hypothetical prote
41	28	77.8	361	2 T38693	hypothetical prote
42	28	77.8	366	2 F83970	probable trna prot
43	28	77.8	370	2 F84151	stage V sporulatio
44	28	77.8	373	2 S54545	response regulator
45	28	77.8	375	2 E81442	hypothetical prote
					probable MCP-domai

Search completed: September 29, 2005, 12:39:52
Job time : 15.5 secs

OM protein - protein search, using sw model

Run on: September 29, 2005, 12:11:58 ; Search time 70 Seconds

(without alignments)
43.893 Million cell updates/sec

Title: US-10-774-147B-35

Perfect score: 36

Sequence: 1 MKYYM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprotc:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	91.7	290	2	Q86PB1	Q86PB1 drosophila
2	33	91.7	316	2	Q87JL5	Q87JL5 drosophila
3	33	91.7	457	2	Q814H6	Q814H6 caenorhabdi
4	33	91.7	477	2	Q8N0R9	Q8N0R9 drosophila
5	33	91.7	484	1	ATE1_DROME	Q96539 drosophila
6	33	91.7	484	2	Q81H08	Q81H08 drosophila
7	33	91.7	485	2	P90914	P90914 caenorhabdi
8	33	91.7	501	1	CP7A_PIG	O46491 sus scrofa
9	33	91.7	501	1	CP7A_RABIT	P51542 oryctolagus
10	33	91.7	504	1	CP7A_HUMAN	P22680 homo sapien
11	33	91.7	513	2	Q76CE9	Q76CE9 gallus gall
12	33	91.7	779	2	Q7RKW9	Q7RKW9 plasmodium
13	32	88.9	565	2	Q8PYC5	Q8PYC5 methanosarc
14	32	88.9	864	2	Q87JL5	Q87JL5 methanosarc
15	31	86.1	58	2	Q9XQ03	Q9XQ03 toxoplasma

16	31	86.1	76	2	Q74KM6	Q74KM6 lactobacill
17	31	86.1	84	2	Q6KSF6	Q6KSF6 mycoplasma
18	31	86.1	108	2	Q84641	Q84641 paramacium
19	31	86.1	165	2	Q97CY9	Q97CY9 clostridium
20	31	86.1	203	2	Q6ABR8	Q6ABR8 propionibac
21	31	86.1	215	1	GRT4_DROME	Q9V96 drosophila
22	31	86.1	239	2	Q8RBB5	Q8RBB5 thermosaneer
23	31	86.1	248	2	Q8KDT6	Q8KDT6 chlorobium
24	31	86.1	261	2	Q81AS2	Q81AS2 plasmodium
25	31	86.1	277	2	Q8NTG5	Q8NTG5 homo sapien
26	31	86.1	297	2	Q9AC14	Q9AC14 ehrlichia c
27	31	86.1	297	2	Q916Z3	Q916Z3 ehrlichia c
28	31	86.1	311	2	Q7Z383	Q7Z383 homo sapien
29	31	86.1	314	2	Q31091	Q31091 rhizobium 1
30	31	86.1	334	2	Q7BUG0	Q7BUG0 rhizobium 1
31	31	86.1	333	2	Q9FKS6	Q9FKS6 arabidopsis
32	31	86.1	399	2	Q97MX2	Q97MX2 clostridium
33	31	86.1	400	2	Q9CWF3	Q9CWF3 mus musculus
34	31	86.1	400	2	Q80UY1	Q80UY1 mus musculus
35	31	86.1	406	1	NPRA_BACST	P43130 bacillus st
36	31	86.1	409	2	Q8N4J0	Q8N4J0 homo sapien
37	31	86.1	461	2	Q84KZ3	Q84KZ3 nicotiana t
38	31	86.1	470	2	Q61LK5	Q61LK5 pterophilus
39	31	86.1	486	2	Q8TP90	Q8TP90 methanosarc
40	31	86.1	509	2	Q94CH1	Q94CH1 zea mays (m
41	31	86.1	529	2	Q7XSQ6	Q7XSQ6 oryza sativ
42	31	86.1	579	2	Q81LA4	Q81LA4 plasmodium
43	31	86.1	586	2	Q7RRU9	Q7RRU9 plasmodium
44	31	86.1	591	1	G6PI_PLAFA	P18240 plasmodium
45	31	86.1	620	2	Q9W708	Q9W708 xenopus lae

Search completed: September 29, 2005, 12:38:18
Job time : 70 secs